Pr. Denis Ducreux's

# DPTOOLS

**Version 5**

# User's Manual

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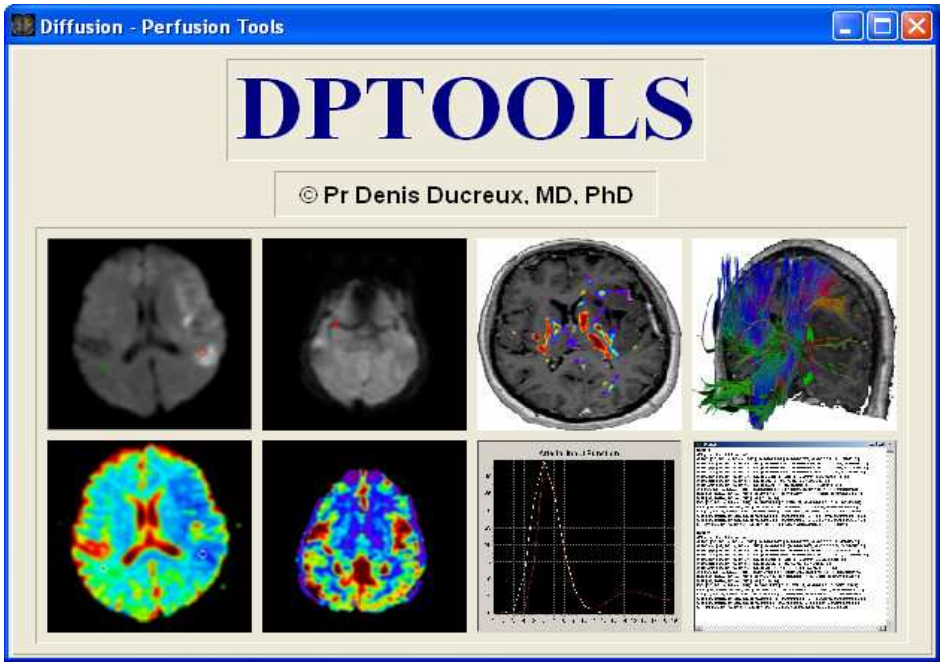

# Requirements

The DPTools software was coded in Delphi, uses the Dr Martin Sanders Optivec © Math Library, and runs on Windows ® systems (Windows Seven, Vista, XP 32 and 64 bits). It was optimized to use multiprocessing workstations (SMP).

At least 1024 MB of RAM are needed to process Diffusion / Perfusion files, and 2 GB for Fiber Tracking with an OpenGL compatible video card.

# Cautions

This software is provided ‘as is’, and is involved in many medical scientific research projects, but is not FDA approved. You can not use DPTools for clinical purposes.

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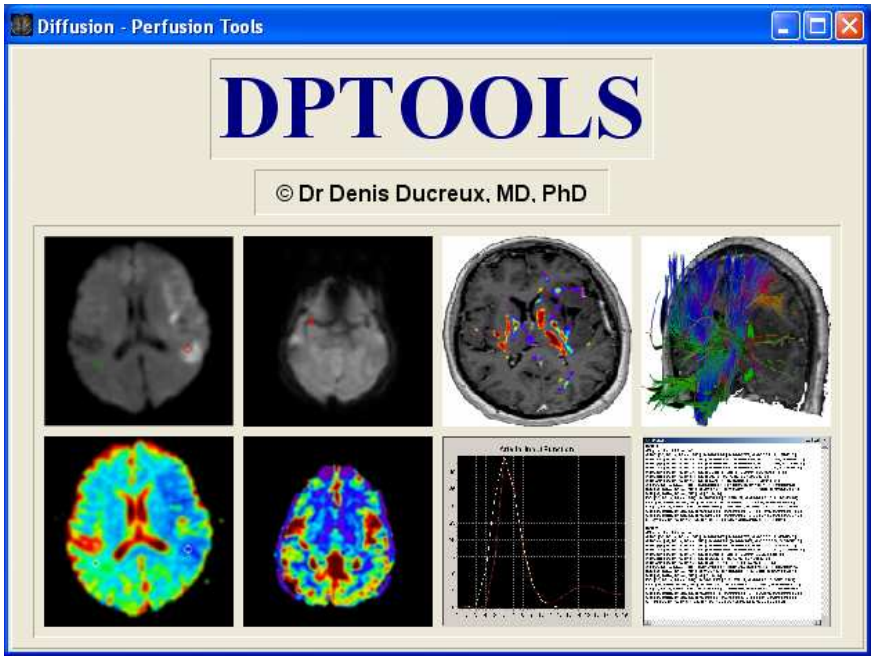
# Chapter I: General Usage Principles

## I. A – Installation, First run

To install the software, use DPTools-Full-Install.exe. The program will be installed in the folder "D:\DPTools" by default, but you can change drive (C:, D:, etc…). It is mandatory to install DPTools in the ***root directory*** (eg c:\DPTools) A shortcut will be generated in the menu Windows. To uninstall the whole program use <<uninstall>>.

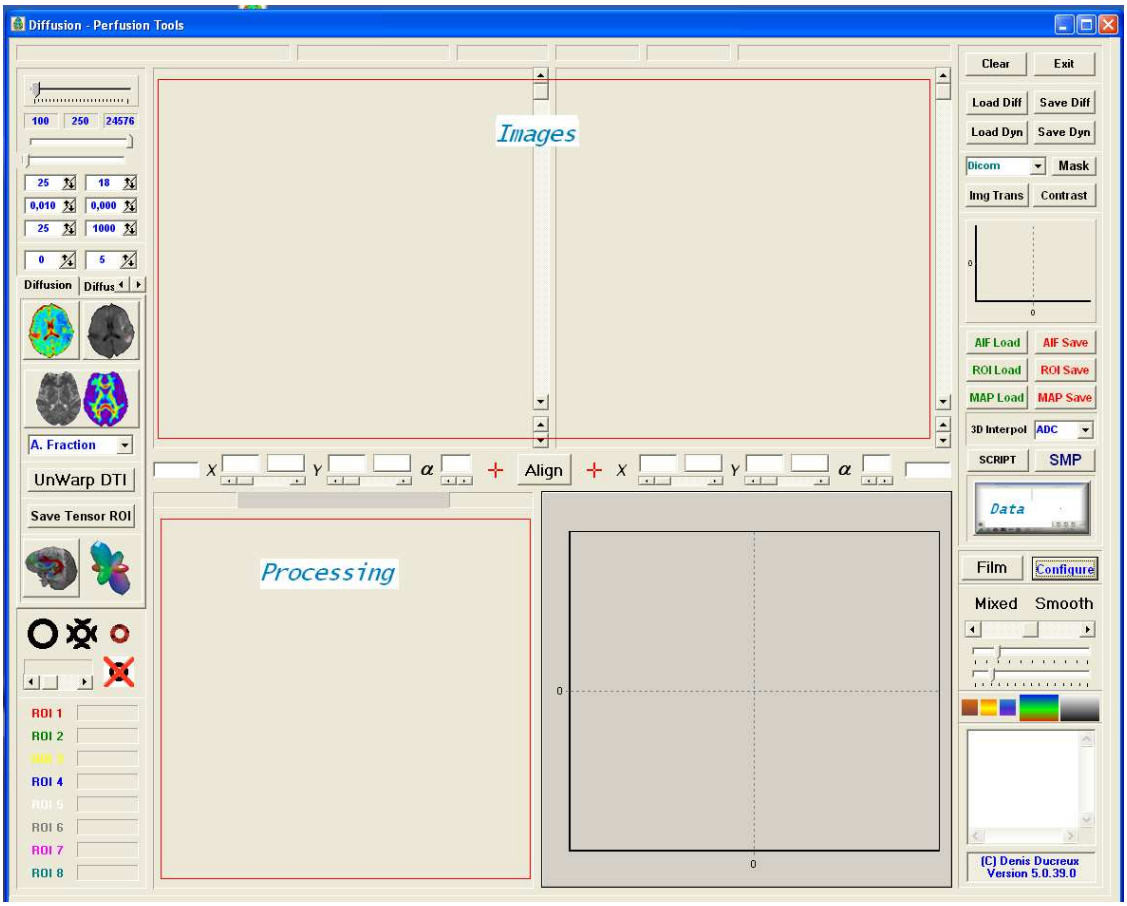
**NB: The data (diffusion, perfusion, etc…) must be located on the same drive as DPTools (e.g. C:, D:, etc…) but you are free to put them in the folder of your choice.**

When software is correctly installed, launch DPTools. The cover page of the software will appear:

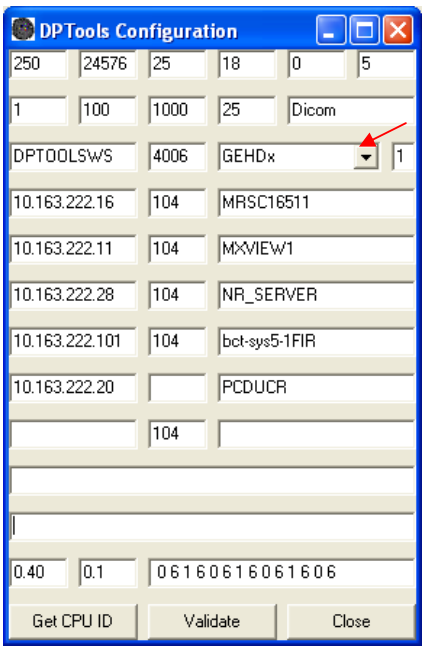



Click on one of the pictures in order to start the program.

In a general way, ‘Left Click’ (LC) executes an action, and ‘Right Click” (RC) selects the action to execute. The main screen of the software is composed of 2 windows with images. One is in the top left of the screen and the other in the top right. The window contains 2 vertical bars with arrows serving to scroll through the images. The bar on the top (the larger one) is the axis of Z, and the bar on the bottom (the small one) serves as the axis of time.



When DPTools is installed on the root directory of your hard disk, you have to configure it before the first time use. Click on the ‘Configure’ button on the right part of the screen.




Many default settings may be set using this configuration utility; just leave your mouse cursor on a label, and a hint will pop up.

It is mandatory to set the right Diffusion Tensor gradient scheme, for exemple ‘GEHDx’ as shown here for the General Electric HDx MRI systems. Other manufacturers (Siemens, Philips) are provided, and you can create your own gradients scheme (see section VI).

If you plan to use DICOM Query/Retrieve and Push functions, you have to set the network nodes (IP Adress, Port, AE Title) as well as the AET and Port of the DPTools workstation.

## I.B – Loading Images

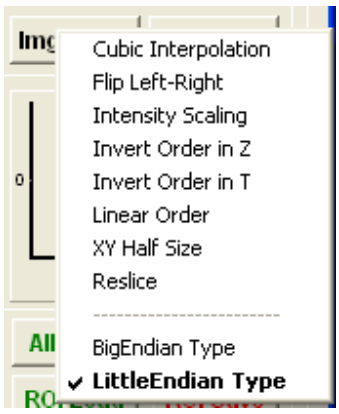
Loading of the images in DPTools is compatible with the following image formats: DICOM, Siemens Mosaic DICOM Files, Genesis, IMA (Siemens), PAR (Philips), Analyze, GIS (Raw format), Pixies and in writing with DICOM color, DICOM grayscale, Analyze and GIS. Before loading the images, you must know their format. DPTools will try to autodetect the correct image format, but may fail.

In this case, Select this format in the menu to the top right of the screen by LC on the arrow on the File Type Selection box.

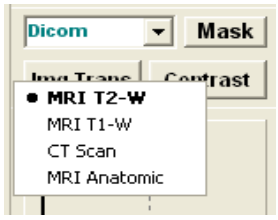
Next to the File Type Selection box are 2 buttons: 'Img Trans' and 'Contrast'. RC on this button to show a pop up menu. LC on an item to select it.

**'Img Trans'**: Basic images post-processing

- *Little/BigEndian*: Selects the type endian of the file. On a PC, the files are "Little Endian', on Sun, they are 'Big Endian'.
- *Intensity scaling*: to adjust luminosity
- *Invert Order*: Classifies the images to load in increasing or decreasing order either in the 'Z' axis or in time ('T').
- *Cubic Interpolation*: Do a tri-linear interpolation on the loaded data
- *Flip Left-Right*: Flip images
- *Linear Order*: When images are stored in time-dependant series.
- *XY Half size*: only half size of the picture is used
- *Reslice*




**'Contrast'**: Image contrast type (MRI T2, T1, CT and Anatomy).



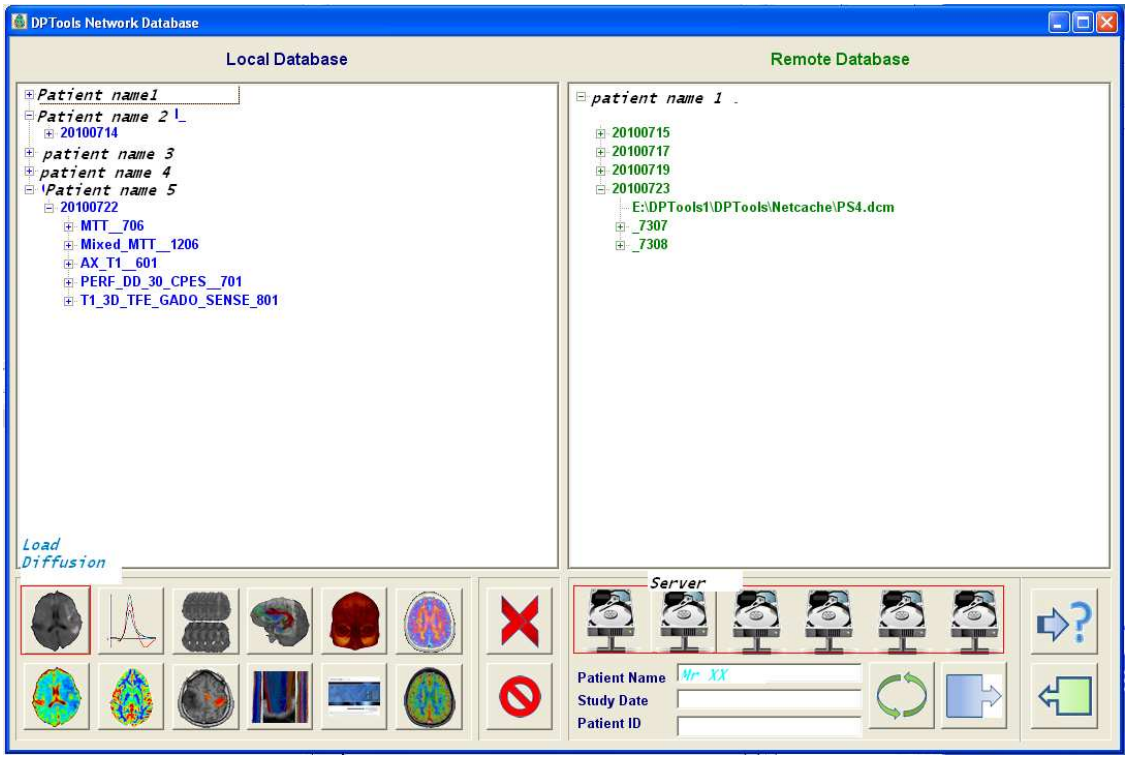
### I.B.a – Diffusion Images

There are two ways to load files, either from a network node (in DICOM), or from a drive.

***1st Technique :***

LC on the button 'Network database'

on the main windows. A new window is opened :

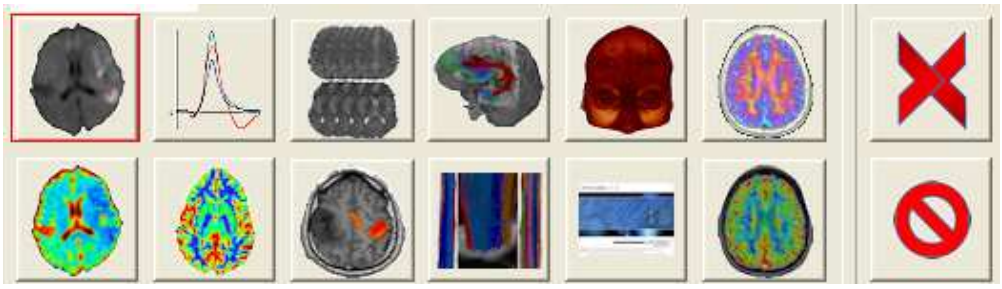



Remote (in green) and local (in blue) exams are in the right or left part of the window. To query/retrieve images, you have to set the dicom AET, IP and Port in DPTools and in the remote network node.

Type in the 'Patient Name' or 'Study Date' field the requested informations, select a network node by LC on it, then click the blue arrow. Results from the search will be displayed. To import a sequence, click on the crosses tree until text with '... \DPTools\...' is displayed. Select the sequence by LC on this text, then LC on the green arrow.

When retrieve process is done, images are displayed in the local DPTools database (left side of the window)

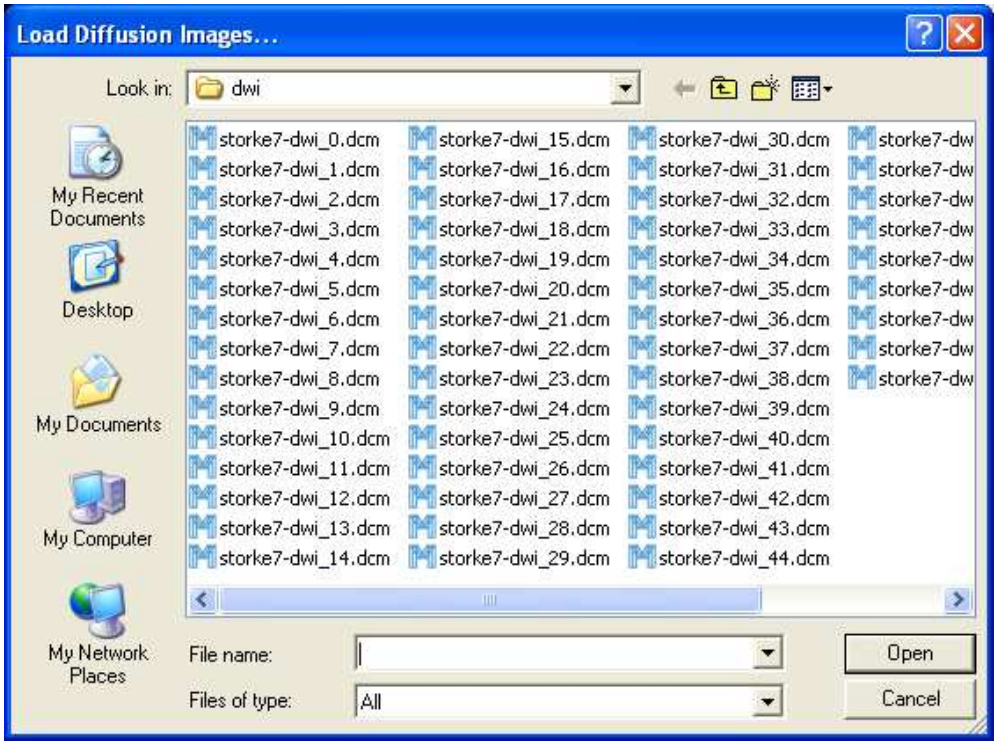
Use the same process of LC on the crosses tree until the text with '...\DPTools\...' is displayed, LC on this text to select it, then LC on the ‘Load diffusion serie’ button (red square on the picture).



***2nd Technique :***

On DPTools home, LC on the button ‘Load Diff’ to load the diffusion images.

Select the group of necessary images (for example, all of the pictures labeled ‘storke-dwi_*.dcm), then LC on ‘Open’.

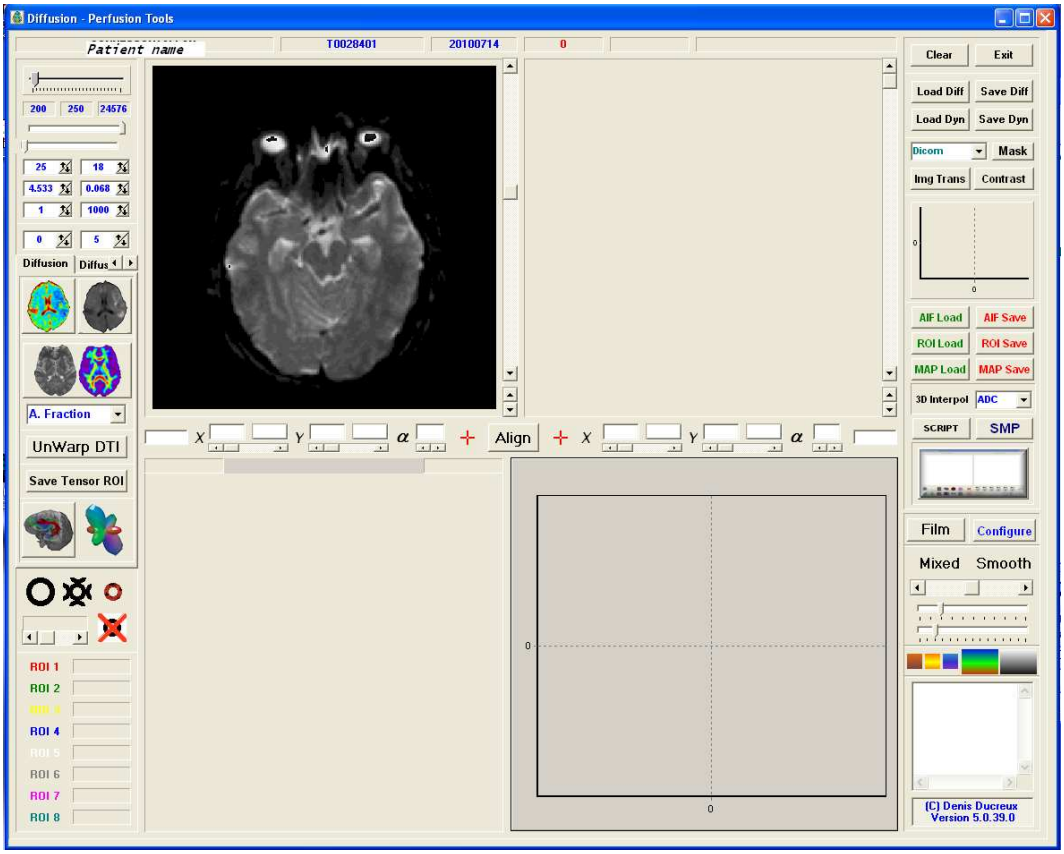



A gauge indicates the progression of the loading of the images.

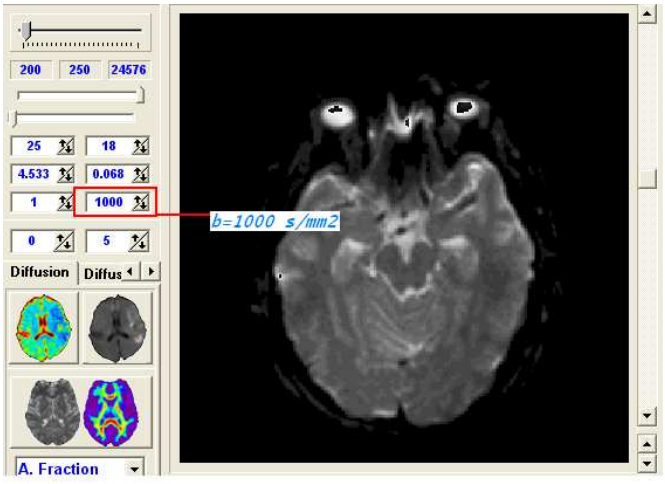
Once loaded, the first image of the first group appears in the image window to the top left.

The software will automatically detect the number of diffusion directions as well as the image order.

**For Dicom format, only dicom images have to be in a specified folder. If other files are present, there will be a loading error message !**




Control if the b value is correct on the left of the screen :

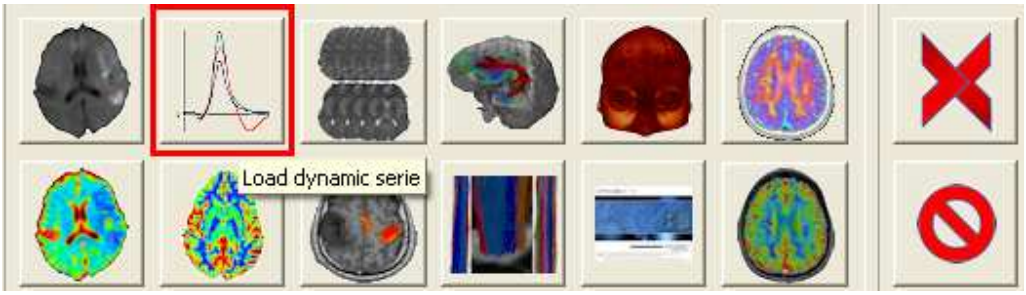


**I.B.b – Dynamic Images**

You must know if these pictures were obtained in T1 or T2. Set the image contrast by RC on ‘Contrast’ button, then LC on T1, T2, etc…

After having defined these parameters, load the anatomical images:

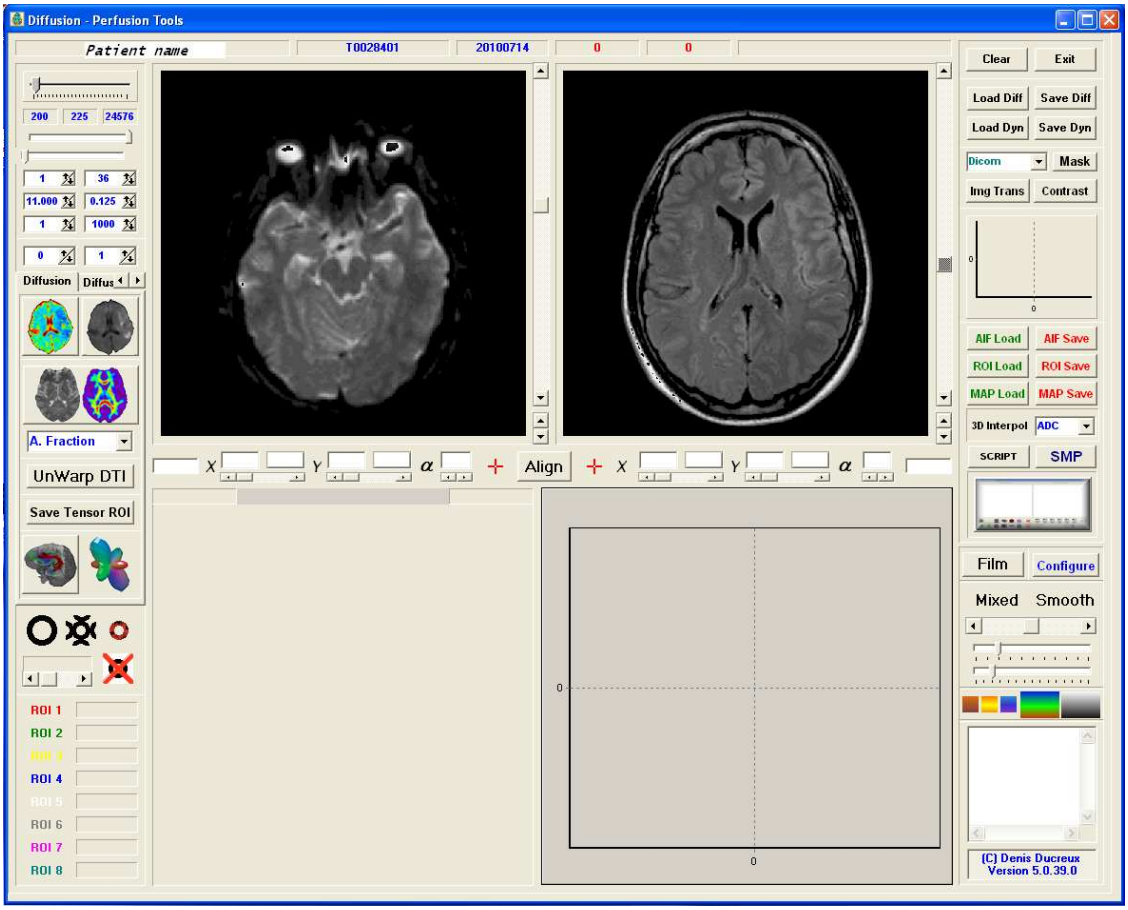
LC on the network database, selects the anatomical sequence and LC on the button 'Load dynamic serie’




2nd method :

LC on the button ‘Load Dyn’ in the top right of the screen, and select all the files (LC on the first file then ‘CTRL A’). Then LC on ‘Open’.

A gauge indicates the progression of the loading of the pictures. Once loaded, the first image of the first volume appears in the image window in the top right corner.



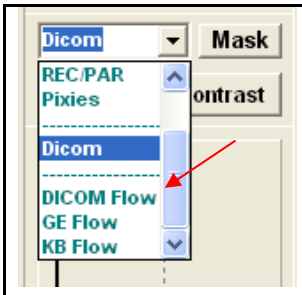

**I.B.c : Loading the images of Permeability/ Anatomy / Reference Images**

The loading of these types of images is based on the same principles as the loading of the images of perfusion (permeability) or diffusion. For example if you want to superimpose ADC maps on T1 volume, first load T1 volume as dynamic, then load diffusion, process the diffusion, and either mixed/MPR-3D then results (see sections III-D and IV-E).

**I. B.d – Loading of flow images:**

Verify that your flow images are encoded on 12 bits.

You must select the adequate file format in the scroll menu in the top right of the screen, while specifying the extension ‘Flow’.

| | |
|---|---|
|  | ‘GE flow’ means Genesis format<br>‘DICOM flow’ means DICOM format. |

Next you must indicate the number of slices to load, and put ‘1’ as the number of volumes. The remainder of process is the same as the one described for the images of perfusion. Select only the images of phases. When the images are loaded, the first one is displayed in the window in the top right of the screen.

## I.C. Display

When the images are loaded, they are displayed in the image windows. The display can seem strange or completely black. This can be due to two reasons: the light of the images is inappropriate or the threshold of the images is too high. By RC on one of the image windows, you have access to a menu of image properties:

- Brightness: to brighten the image.
- Zoom: to enlarge a portion of the image.
- FOV: to enlarge the entire image.
- Cursor Position: to position the cursor on a section of the image.

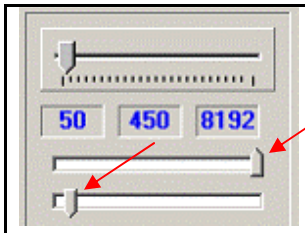
### I.C.a. Windowing / Thresholding

#### I.C.a.1. Brightness :

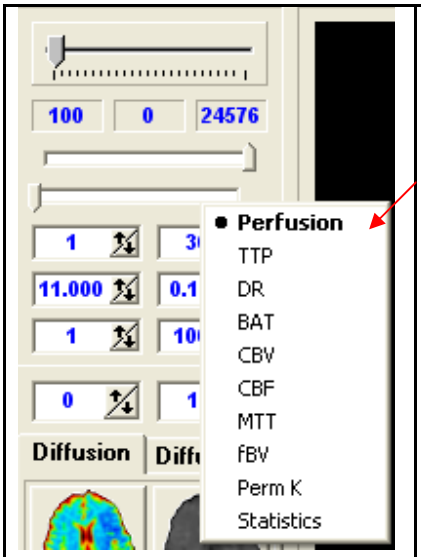
By LC on Brightness after having RC on the image window you can change the brightness of the image. Keep the left mouse button down and move your mouse. You'll see the image get brighter (move toward the top left or darker –toward the bottom right).

#### I.C.a.2. – Threshold:

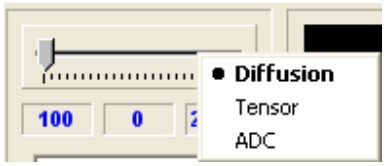
The threshold of images consists of putting to 0 every pixel that has a value outside of the threshold values. The threshold of images is done by moving the cursors of the tab "Threshold' on the top left of the screen.




The 'Diffusion Threshold' refers to the image window in the top left. The "Low" and "High Perfusion Threshold" to the image window in the top right of the screen.



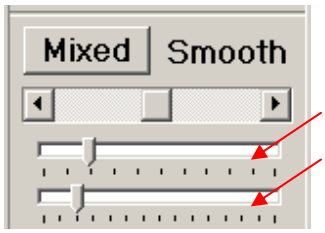

When RC on the threshold bar, you get access to a pull-down menu that allows you to set a threshold for the diffusion/perfusion images or the charts when these are being calculated.

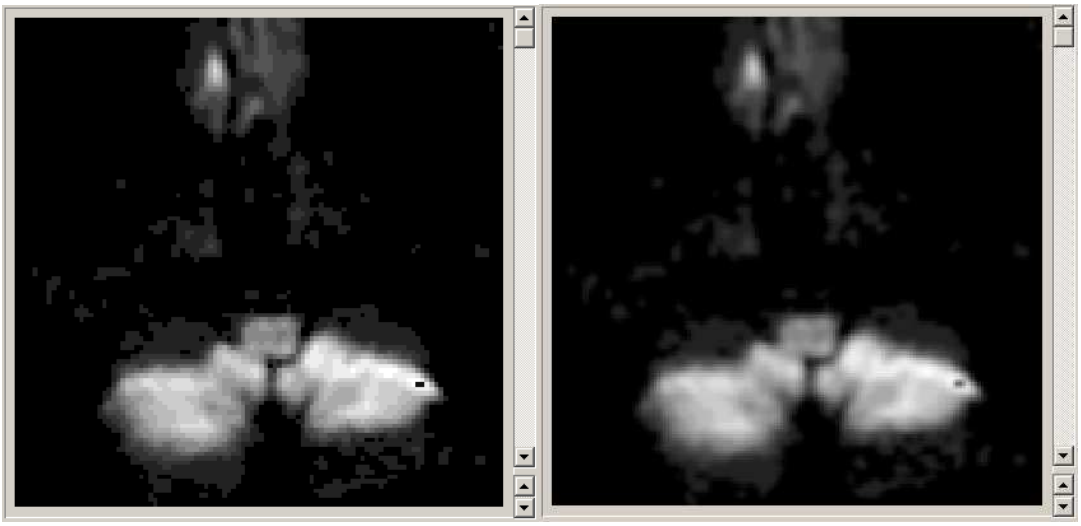



**I.C.b. Changing the image quality:**

By clicking the button ‘Smooth’ in the bottom right of the screen, all images are smoothed with a spline filter, improving the quality and reducing the pixelization effect (especially visible in images with a weak matrix or that are zoomed in strongly.

You can adjust the additional Gaussian smoothing using the scrollbars near the ‘Smooth’ button.



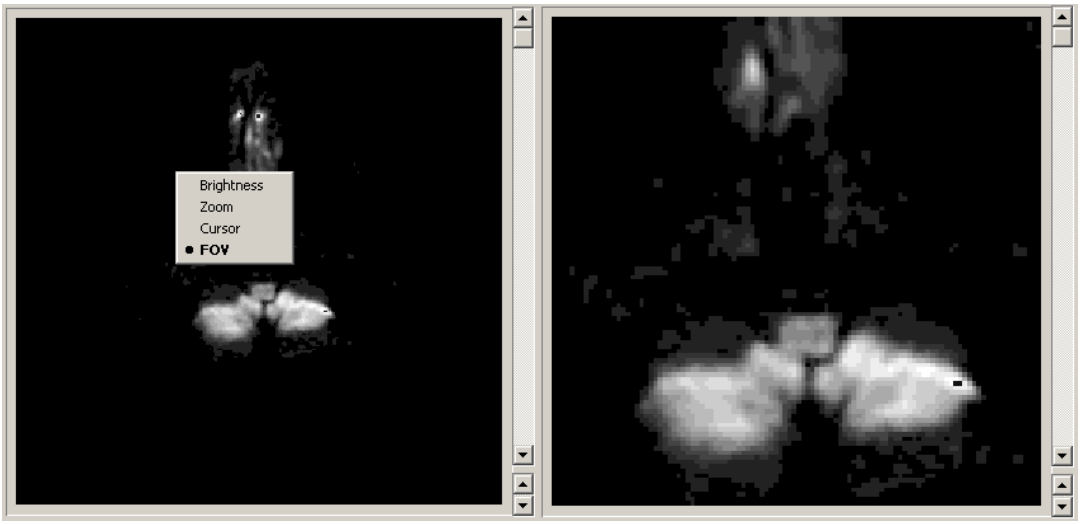


**I.C.c. – Zoom in/out on images:**

You can either enlarge the whole image (FOV) or use a magnifying glass to enlarge a part of the image temporarily (Zoom).

**I.C.c.1. FOV – Field of View:**

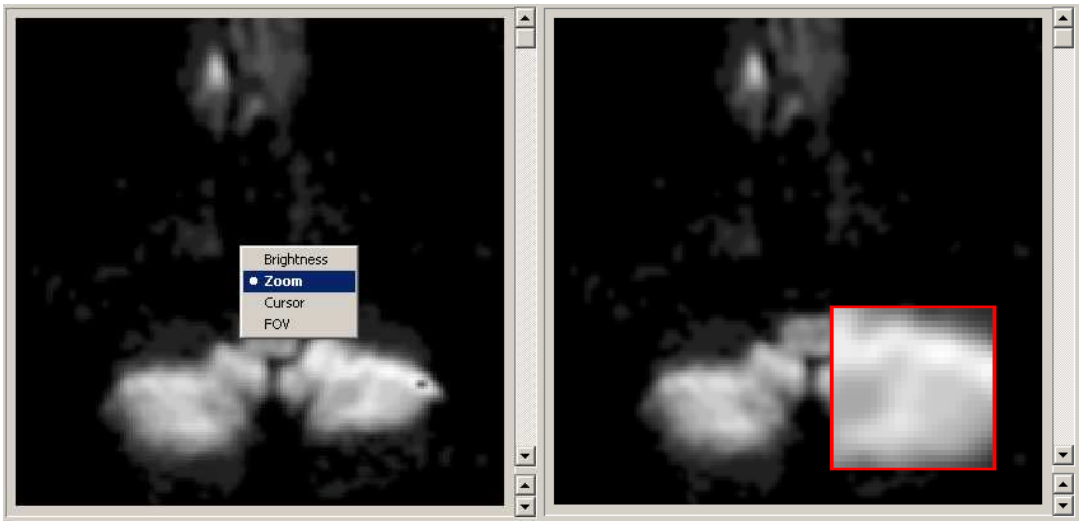
RC on the image window, then LC on FOV allows you to enlarge the image. To do this, keep the left mouse button down while you move your mouse. You'll see the image get bigger (cursor to the top left) or get smaller (cursor to the bottom right).




The enlargement values of the FOV are indicated under the image.

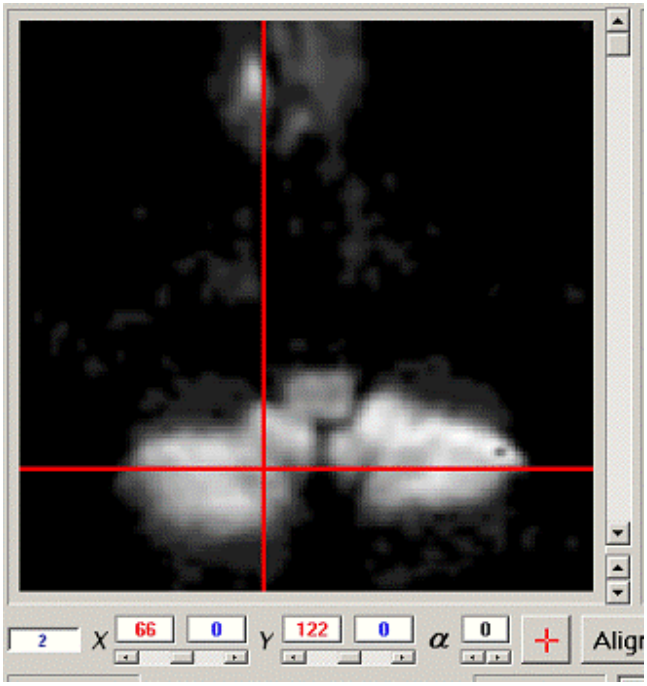
**I.C.c.2. Zoom:**

RC the image window, then LC ‘Zoom’ allows you to enlarge part of the image by using a magnifying glass. To do this, keep the left mouse button down on the image while moving your mouse. You’ll see a part of the image enlarged surrounded by a red square.



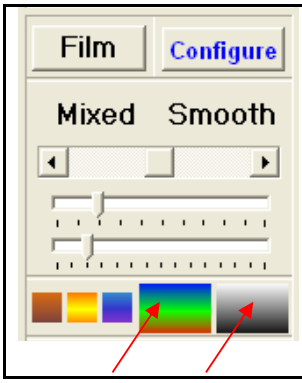

**I.C.d. Cursor:**

RC on the image window and then LC on the 'cursor' to get the coordinates of the cursor proportionate to the size of the image. You can make the cursor visible as a red cross by clicking: ….



You can re-center the image in X and Y and you can pivot it (α) by moving the horizontal cursors. To make your selection, LC “align’. To de-activate the red cross, LC on it.

**I.C.e. Colors:**

| | |
|---|---|
|  | You can choose to view the image in B&W or in color. LC the button with the color gradient to see in color, the one avec the B&W gradient to see B&W.<br>Preset display color scales are also provided (from red to blue), next to the Color / B&W buttons. |

You have some parameters indicated on the left of the screen:

## I.D - Regions of Interest:

The Regions of Interest (ROI) can either be drawn automatically following a squared circle of variable sizes or manually, by circling the Region of Interest. There are a maximum of 8 ROIs that can each contain a large number of pixels.

The different ROIs are represented by a unique color code (red, green, yellow, etc.) which allows you to find them on the image. The values of each ROI are calculated depending on the calculation (mean, deviation, minimum, maximum).

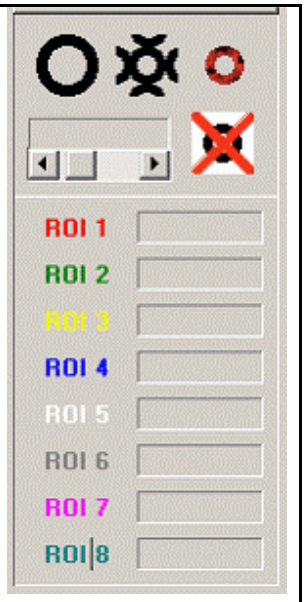
To place a ROI you have to first select the 'Cursor' function in the image window (1.C.d.).The ROI functions are on the bottom left of the screen.

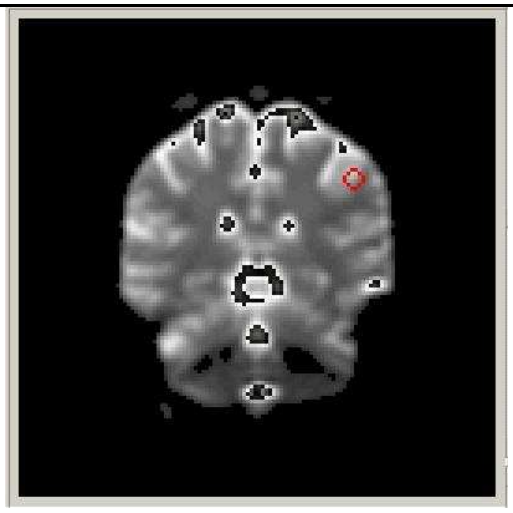
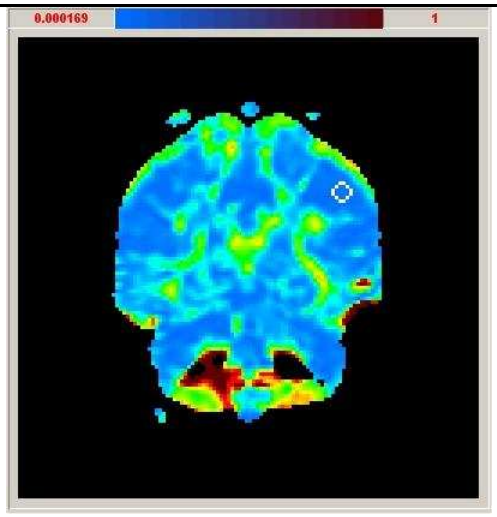
### I.D.a. Automatically round ROI

To place a ROI, LC the icon:

Then choose the surface of your ROI by moving the cursor on the horizontal bar. The surface of the ROI will be visible above (here 77 mm2).

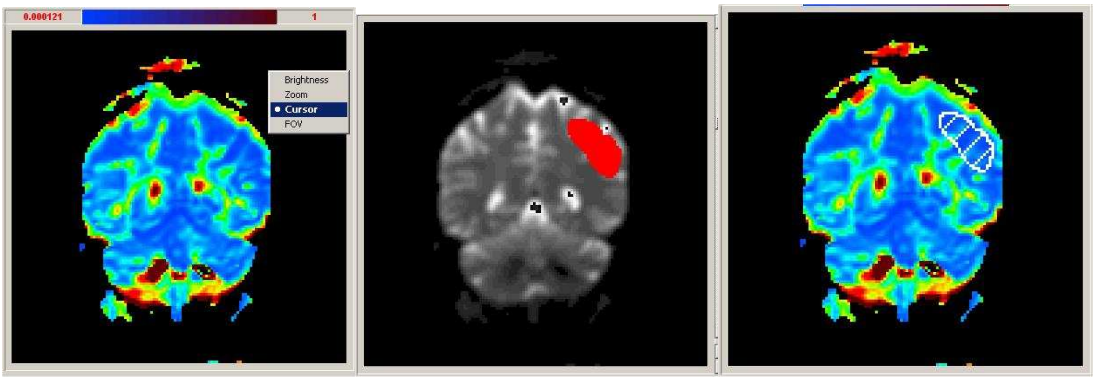

If you want to move an ROI, LC on in the image window while moving your cursor.



| | |
|---|---|
|  |  |
| Once active, position a ROI by LC the image window. | The corresponding ROI is also visible in the calculation window (white circle). |

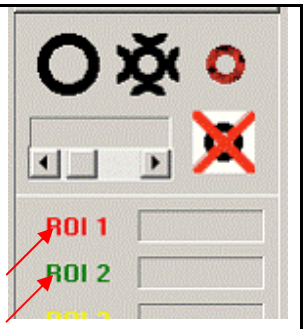
**I.D.b. Manual ROI**

You can draw a ROI manually. LC the image window and choose ‘Cursor’. Do not select ROI (don’t LC ). Keep the left mouse button down, push ‘shift left’ at the same time and circle the selected area by moving your cursor.



The selected area will then appear following the number of the color of ROI in the image window and in white stripes in the calculation window.

**I.D.c - Deleting parts of all of ROI:**

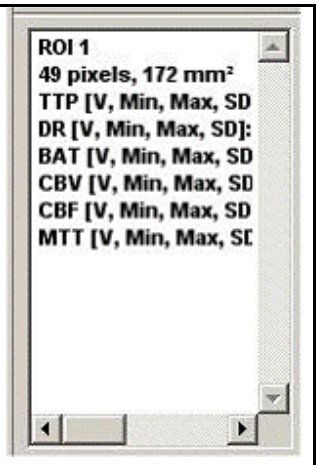
| | |
|---|---|
| You can delete a ROI by LC on the color code of the ROI in the bottom left of the screen.<br><br>To delete all ROI, LC on: |  |

**I.D.d. exporting/importing ROI**

You can save the drawn ROI and load them later. Click on 'ROI load' to load or on 'ROI save' to save the ROI either in Analyze or Raw format in the import/export zone at the right of the screen.


**I.D.e. Display and export of results:**

Once the ROI is positioned the obtained values are displayed in the result window on the bottom right of the screen. Different values are displayed according to different calculations.

| | |
|---|---|
| • You can enlarge this result window by double-clicking it; another result window will then appear in the middle of the screen. It can be behind the main screen. You only need to move it to find it.<br>• You can save the results as a text file or as an Excel file by typing F1 when your cursor moves onto the result window. |  |

**I.D.f. How to create a mask**

There are to ways to create a mask. The first method uses a defined circle of the area you want to keep or delete by using the manual ROI function (1.D.b.), then push F3, F4, F6 or F7 once while moving the cursor of the mouse on the pertinent image window.

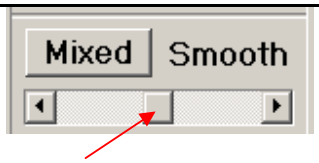
- F3 – keeps the selection that is circled and erases the rest of the visible slice.
- F4: erases the selection and keeps the rest on the slice.
- F6: keeps what has been circled and erases the rest on the visible slice in all the volumes
- F7 Keeps what has not been circled and erases the rest on all the slices of all the volumes.

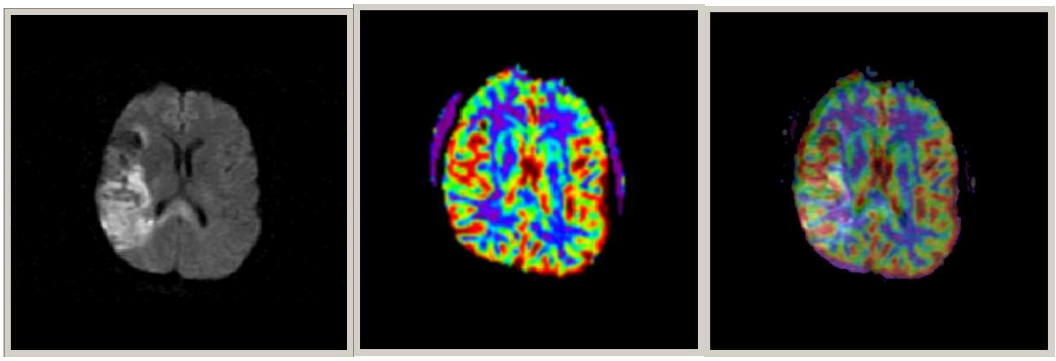
The second method uses a extract brain mask by LC on the ‘Mask’ button

near the Image type combo-box. This function is only working with T2-w MRI sequences.

## I.E. Images Overlay

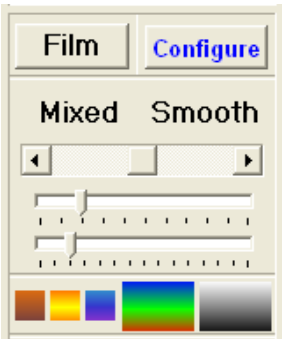
This function allows you to superimpose the image of the image window on the top left of the screen with the image of the calculation window in the bottom right. You can stack with or without smoothing activated (button ‘Smooth’, 1.C.b.), for example Diffusion and Perfusion results.

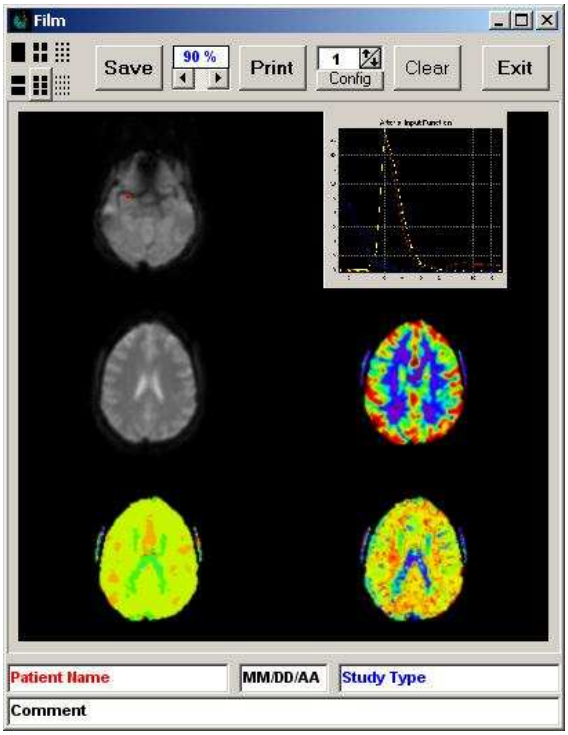
| | |
|---|---|
| LC on ‘mixed’ on the right of the screen.<br>The transparency of the images can be adjusted with the horizontal cursor. |  |



## I.F. Filming and saving images

You can save and print the images of the image window, the calculations and the curves obtained in the curves window in the bottom right of the screen.




LC on 'Film' in the bottom right of the screen. The Film Composer window will appear in the center of the screen.

You can select the size of the images (1, 2, 4, 6, 12, 16).

The text zones hold the notes available as well as the name of the patient and date of the study.

To send an image to the Film Composer you have to position your cursor on an image window (calculation or curves), hit F1 and move your cursor (for all images, hit F2).

- To print your Film Composer, LC 'Print'
- To select the printer to use, LC 'config'
- To save your Film Composer as a JPEG, LC 'Save'
- To adjust the export quality of your Film composer, move the cursor next to the 'Save' button.
- To delete the Film composer, LC 'Clear'. Changing the image format will not erase the text fields.
- The film composer can easily be hidden behind the main screen. You just have to move the various open windows around to find it.

## I.F. Scripting

You can automate the post-processing: LC on the button ‘SCRIPT’ to register


Scripts are text files designed using file type (Dicom, GIS, Analyze, ...), contrast (T2, T1, CT, Anat), Low Threshold, High Threshold, AIF type (LOCAL, GLOBAL) and position (x y z), and functions (FILE, PFILE, MSAVE, TIMESHIFT, DIFF, PERFL, PERF, TENS, CLEAR, ROI x y z, aso...). It must end by 'EOF'.

Here is an example :

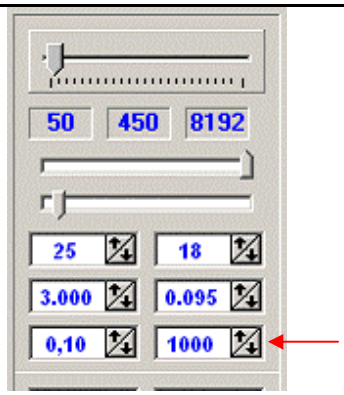
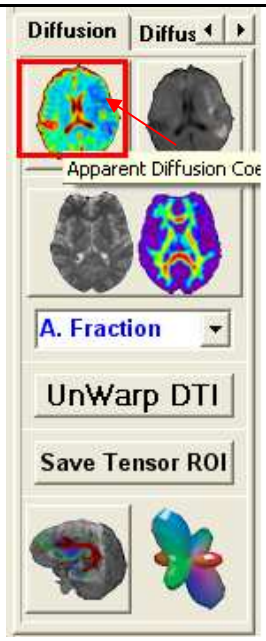
```
GIS
T2
450
8192
LOCAL
FILE
\batch\temoin10
TIMESHIFT
AIF
71
66
5
PERF
ROI
71
68
9
CLEAR
PFILE
\batch\PWITemplate\T1Coreg
AIF
73
58
7
PERFL
MSAVE
CBV
GIS
\batch\PWITemplate\T1Coreg-CBV
CLEAR

EOF
```

# Chapter II: Calculating Diffusion

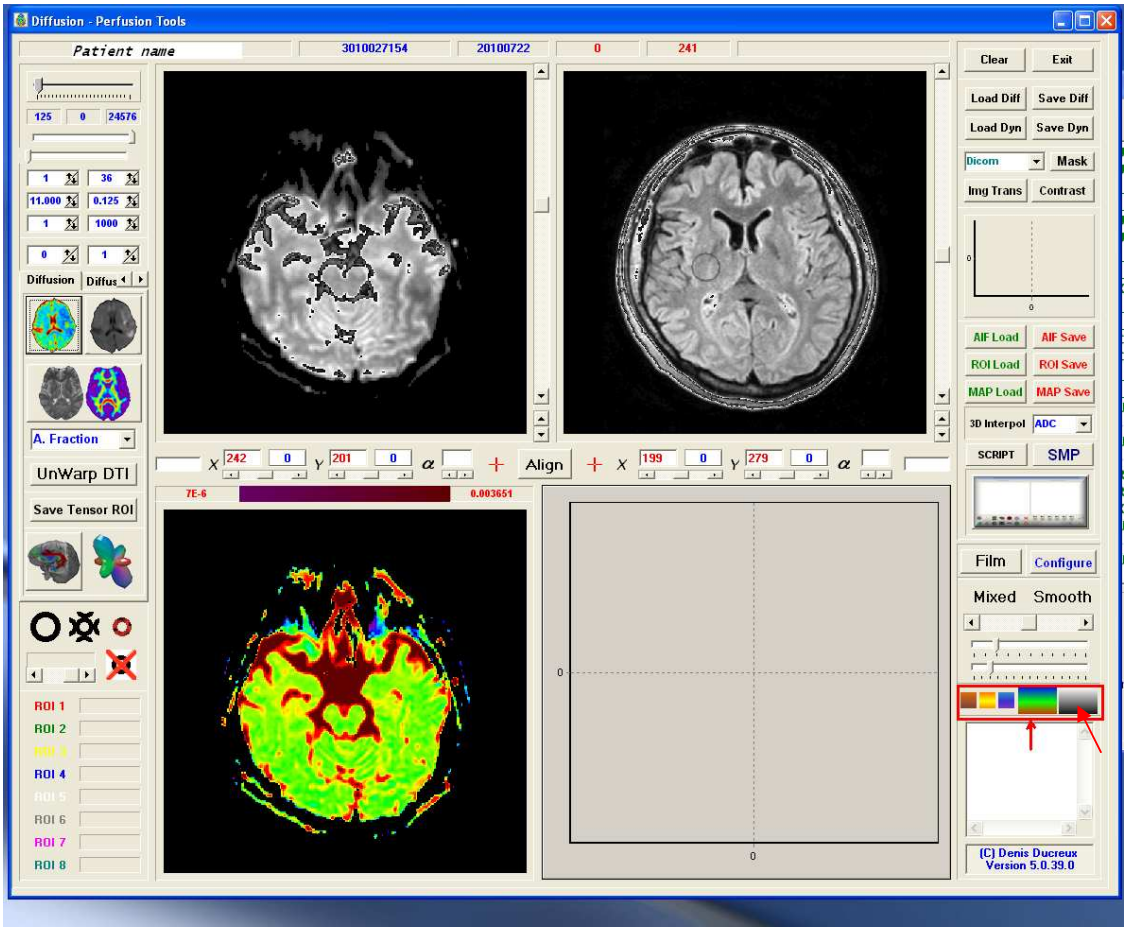
The process of calculating diffusion is found under the 'Diffusion' tab on the left of the screen.

### II.A. – Trace

Before loading the trace images you have to choose the correct image format.

| | |
|---|---|
|   |   |
| choose the appropriate value of b in the corresponding field (here 1000) | LC on the 'ADC' button to calculate ADC. |

You have to see the ADC mapping in the calculation window.




If you wish to change the window coloring, RC on the calculation window, then select 'Brightness' by LC and then LC the image by moving your cursor (I.C.a.), or use the preset color-scales buttons (right part of the screen).

Likewise you have access to the other function of 'Cursor' for the positioning of ROIs (I.C.d.), 'Zoom', and 'FOV' for the enlargements (I.C.c.). when you change FOV of the calculation window, the FOV of the corresponding image window is automatically adjusted.

You can also change the diffusion threshold by moving the position of the 'Diffusion Threshold' cursor in the top left of the main screen.

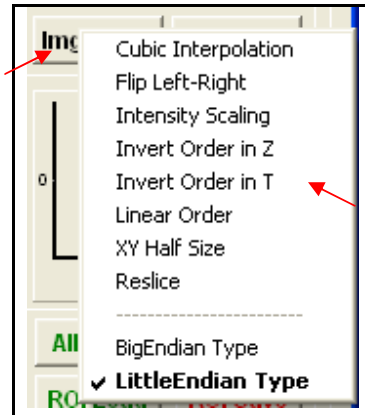
## II.B. – Tensor

The images of diffusion tensor are composed of at least 7 groups of images (6 DTI and the b0). Before loading the tensor images you need to select the correct image format. Number of gradients will be automatically detected.

### II.B.a. – Loading the images : Inversion

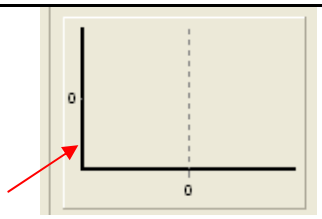
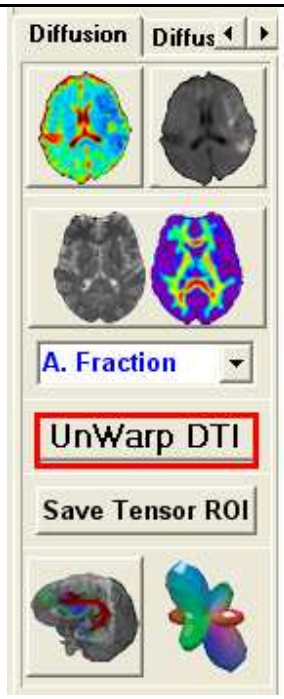
If you calculate the tensor image in order to track the fibers you need 2 sets of images: DTI and anatomy (see II.B.5.)

Make sure the first image that becomes visible in the left image window is always in the same position as the corresponding anatomical image (cranial or caudal, but identical as to anatomy and DTI).

| | |
|---|---|
|  | If the first image is inverted you need to delete the loaded images by LC 'Clear' in the top right of the main screen, RC the 'Img Trans' button, LC on 'Invert Order in Z' then re-load the images as described before. |

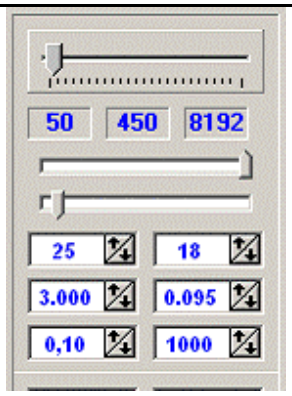
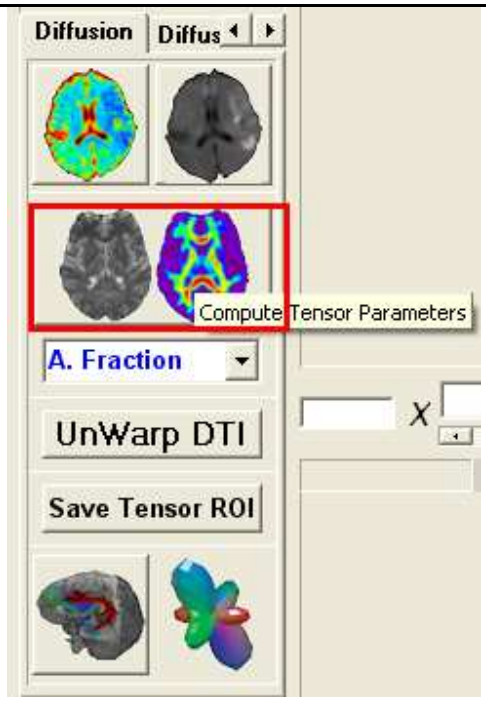
### III.B.b. Correction of EPI distortion

You can correct your DTI data in 2 ways

| | |
|---|---|
| Correction of distortions due to diffusion gradient ; double-click on then curve graph in the top right of the screen. |  |
| Correction of distortion due to the EPI sequence: this correction requires a phase map. Click on 'Unwarp' in the left of the screen under the 'Diffusion' tab. |   |

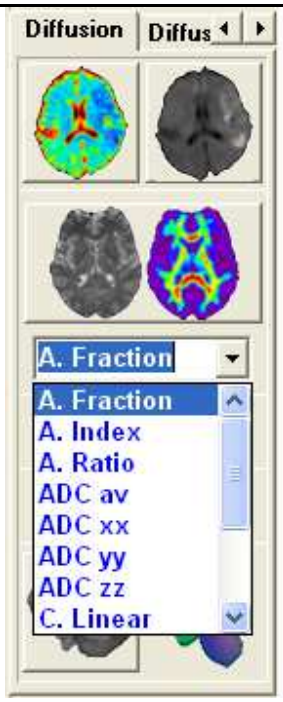
**II.B.c. – Processing**

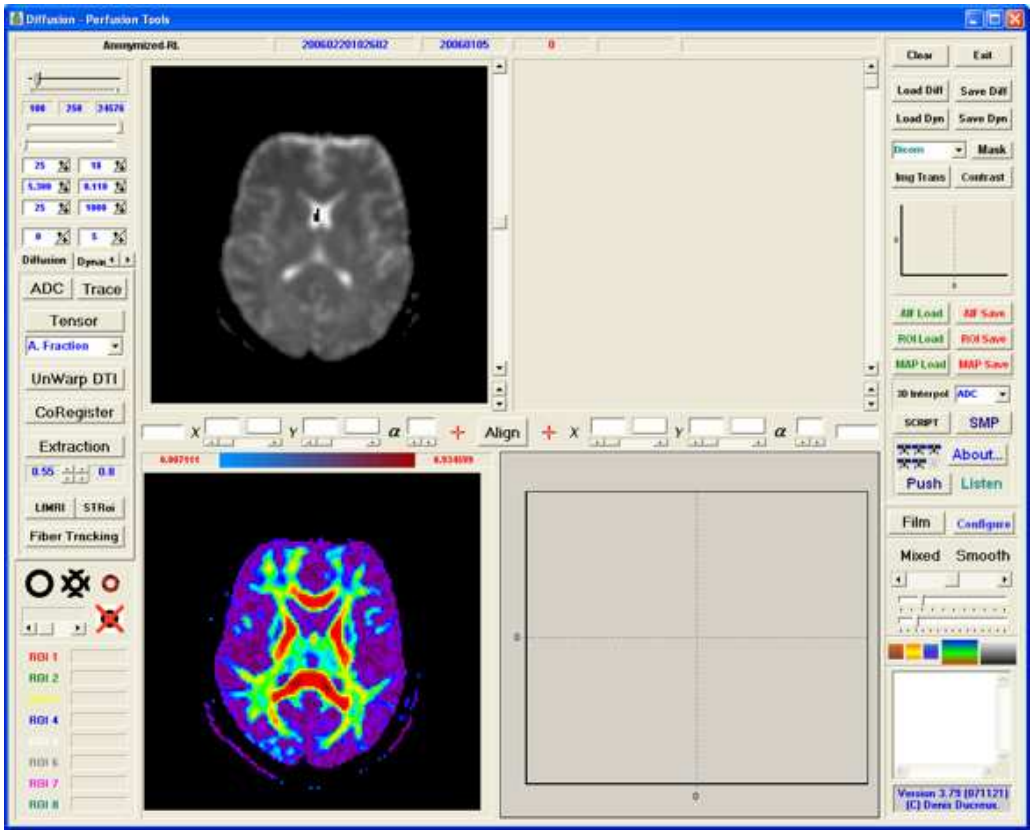
Once the diffusion images have been loaded correctly you can make your calculations. The 'tensor' calculates the real values and the real vectors of the acquisition matrix and calculates the Anisotropy fraction, the Anisotropy ratio, the Volume Ratio, the ADC in the main axes, the mean ADC etc… The 'Trace' button will compute the trace image from the DTI set after having computed the FA, VR, etc….

| | |
|---|---|
|  |  |
| Choose the correct value of b in the corresponding field (here ‘1000’) | LC on the ‘Compute Tensor Parameters’ button to calculate the Anisotropy Fraction, etc… |

**II.B.d. – Display of the results**

You need to see the selected mapping (default is Anisotropy Fraction) in the calculation window.

| | |
|---|---|
|  | You can display another map (for example (Anisotropy Fraction). LC on the scroll bar under the 'Compute Tensor Parameters' button in the diffusion tab on the left of the screen and then LC the item you wish.<br>The map will update automatically. |



Take care of the FA results as they reflect the correct DTI gradients scheme. Corpus callosum have to be in red like in this image. If not, your DTI gradient scheme may be wrong, and you have to check the 'Configure' button to see if declared DTI gradients match your MRI system.

If you want to change the color scale of the window, RC on the calculation window, then choose 'Brightness' by RC, then LC on the image while moving your cursor (I.C.a.)
In the same way you can access the other 'Cursor' functions for the positioning of ROIs (I.C.d.), 'Zoom', and 'FOV' for the enlargements (see I.C.c.). when you change FOV of the calculation window, the FOV of the corresponding image window is automatically adjusted.
You can also change the diffusion threshold by moving the position of the 'Diffusion Threshold' cursor in the top left of the main screen (see I.C.a.).

**II.B.e. – Exporting/Importing maps**

Once the calculations have been made, you can save the results.

- Saving in the 32 bit 'RAW' format will allow reloading the results for new calculations
- Saving in the DICOM color or B&W format (depending on the display of the images in color or B&W, see I.C.e.) to integrate into a PACS for example.

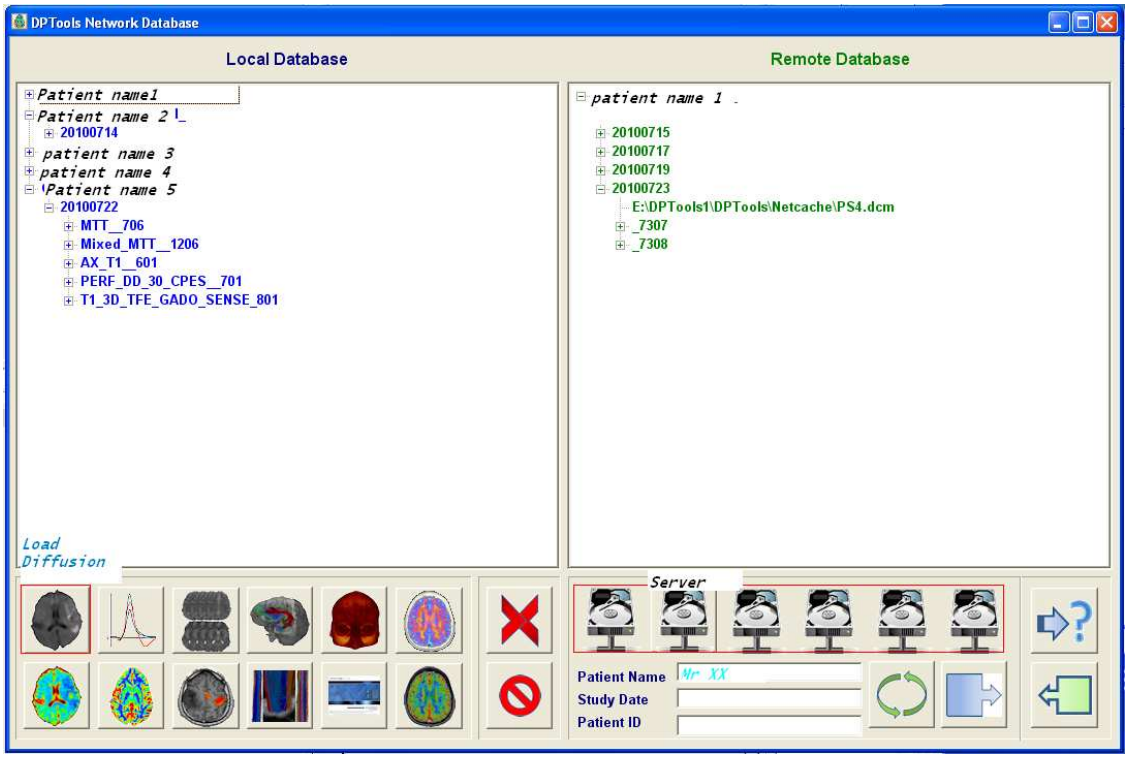
- Choose the type of map for export by LC the scrolling menu in the bottom of the import /Export zone (here 'ADC')
- LC 'Map save' to export the maps
- Choose the format DICOM or GIS and click 'Save'
- LC 'Map Load' to load the maps. Be careful, only the maps that were saved as RAW Gis can be re-read.

**II.B.f. – FiberTracking**

Once you have loaded and calculated the DTI images, you have to load the anatomical images in the window on the top right of the screen.

**II.B.f.1. – Loading anatomy**

LC on the button 'Network database' to load the diffusion images. A new window is opening :




Import the Diffusion images from server in the database. Select the right sequence and LC on button ‘load diffusion serie’.

**or**

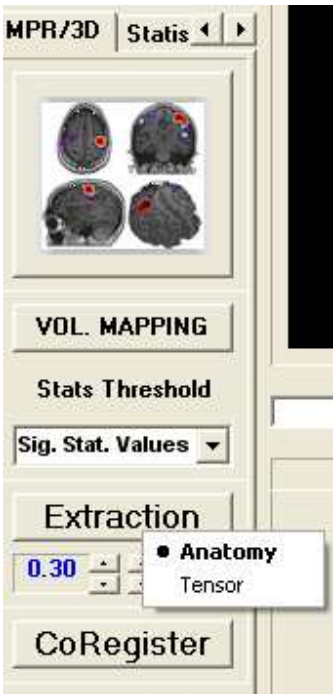
To load the anatomical images, choose “MRI Anatomy’ in the pop up menu of the ‘Contrast’ button (RC then LC). Then check in the parameter zone that the number of slices corresponds to the indicated number and that the number of volumes is set to ‘1’. (see I.B.b.). then LC ‘Load Dyn’ and select your anatomical images.

The DTI images and the anatomical images must have the same cranio-caudal orientation (identical 1$^{st}$ slice position). If the DTI images don’t correspond to the anatomical ones, invert them using the previously described method and re-load your anatomical images.

NB: Do not LC ‘Clear’ because this will erase all your calculated images.

### II.B.f.2. Cortex extraction

The extraction algorithm of the brain used is BET (FSL, see 'References').




To extract the brain based on the anatomical images, LC on 'Extraction' in the MPR/3D tab on the left of the screen.

You may also extract brain using FA values by RC on 'Extraction' then LC on 'Tensor'. You'll have to set the FA thresholding values to do so.

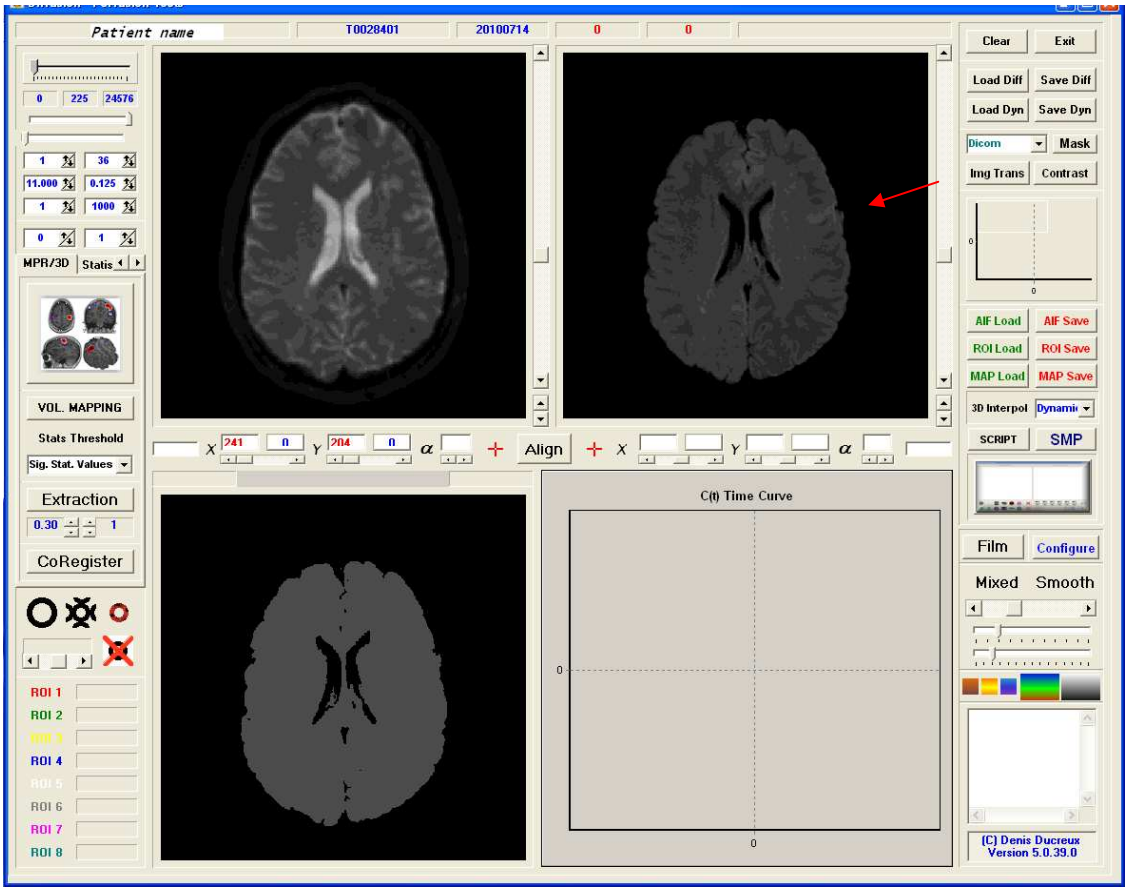
You can change the extraction parameters by changing the values of the underlying fields (here 0.30 and 0.8)

- The first field (here 0.30) corresponds to the degree of smoothing of the extraction
- The second field (here 0.8) corresponds to the value of the median filter used for binarization.

The files created correspond to the extracted brain (brain.hdr' and 'brain.img') and to the binarised mask of the latter ('mask.hdr' and 'mask.img') and are saved in the anatomy folder '…\Brain\'.

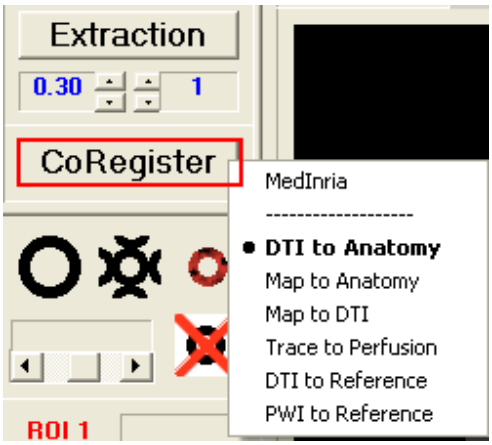
The brain extract appears in the calculation window; you can scroll through the slices by moving the horizontal arrow on the right of the right image window. When you regulate

your brain extraction parameters, make sure that the brain folds in the final image are visible from the vertex to the temporal lobes.




### II.B.f.3. DTI / Anatomy registration

The adjustment algorithm used is the FSL algorithm (see References)

| | |
|---|---|
|  | • Select the type of co-registration by RC 'CoRegister' in the 'MPR/3D' tab, then load the anatomical images.<br>• When the images are loaded, LC 'CoRegister' on the left of the screen in the 'MPR/3D' tab.<br>• The DTI images are adjusted to the anatomical ones and a transformation matrix 'b0.mat' is created. All files are saved in the tensor folder '…\DTI\'. |

**II.B.f.4. FiberTracking**

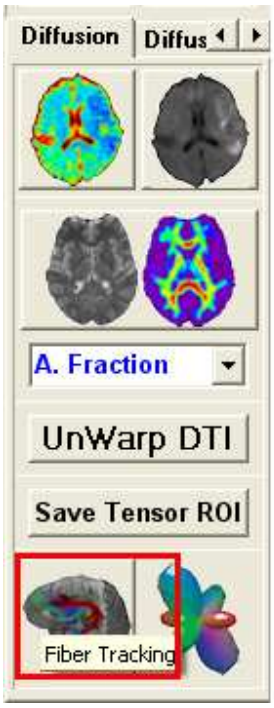
To perform fibertracking, MedInria must be previously installed in the '\DPTools\MedInria' folder of your hard disk (see http://www-sop.inria.fr/asclepios/software/MedINRIA/).

When the DTI and anatomical files are loaded and adjusted, the ROI have been defined and the cortex has been extracted, you can start tracking the fibers.

### II.B.f.4.a. Carrying it out

To track the fibers, RC on ‘Fiber Tracking’ in the ‘Diffusion tab on the left of the screen.

to select the image orientation (Axial, Sagittal or Coronal) by LC, then LC on ‘Fiber Tracking’




Once obtained, the results stay available in the folder ‘…\DTI\’.

### II.B.f.4.b. – Loading of an earlier calculation

You can re-use DTI’s, anatomies etc. that have already been calculated. Simply load the DTI files (see I.B.a.2.) then LC ‘FT’ in the ‘Diffusion’ tab on the left of the screen.

# Chapter III: Calculating dynamic images

Calculating dynamic series is found under the 'Dynamic / Activation' tab on the left of the screen.


## III.A. – Perfusion

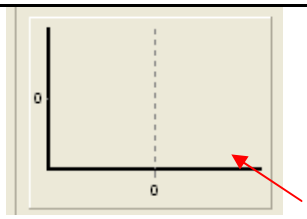
Before loading trace images, you need to select the correct image format.

### III.A.a. – choosing the type of image (T1/T2/CT) and loading

The perfusion calculations are based on the evolution of the signal in time. This signal evolves differently depending on the method you use, MRI T1 or T2, or CT. You have to choose this method (MRI T1-w or T2-w, or CT ) before loading the perfusion images by RC on the 'Contrast' button on the top left of the screen until the right option appears. Then you can load your images as described in section I.B.b.

### III.A.b. – Spatial Coregistration

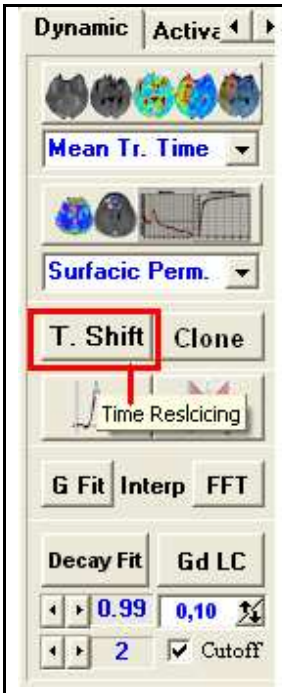
The algorithm of space adjustment used is the one by Woods. It allows for reduction of side-effects due to movement by the patient.

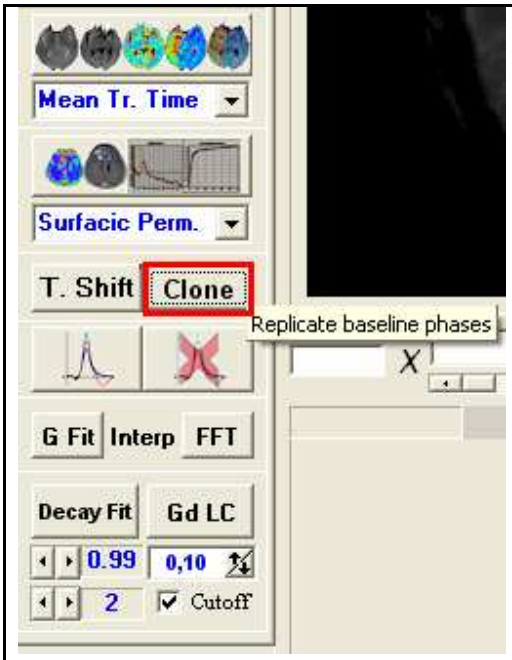
| | |
|---|---|
| To apply the adjustment, double-click on the Graph. A registration graph will appear in the underlying window. |  |

### III.A.c. – Temporal Coregistration

The series of perfusion obtained in MRI are usually intertwined. This means there is a substantial time difference of about ½ TR between the first slice and the middle slice.

If the TRs are long (>2s), it is strongly recommended to adjust the series for time in order to correct the time difference at acquisition.

| | |
|---|---|
|  | In the 'Dynamic' tab, LC 'T. Shift'. This will launch the time adjustment algorithm based on a bilinear interpolation of the signal.<br>NB: the time adjustment has to be done first - before the space adjustment and the other calculations of perfusion such as the selection of AIF etc. |




In the ‘Dynamic’ tab, LC ‘Clone’.

You modify the Baseline.

RC on the button “clone” and choice :

- *Av baseline clone:* to average baseline
- *Baseline clone:* to spread baseline
- *Extrapolate endline:* if the contrast injection is not over before the end of the sequence, you extrapolate the end of the curve.

You can select the kind of filter: Gaussian Smooth, Law Pass Filter or LP filter Display.

**III.A.d. – Elimination of recirculation**

The elimination is obtained by adjusting the arterial and capillary functions by a model combining de functions ‘power’ and ‘exponential’.

The adjustment of the data has to be selected before any calculation of perfusion and before the selection of AIF.

LC on ‘GFit’ under the ‘Dynamic’ tab on the left of the screen


This adjustment of data sometimes generates wrong results if the adjustment does not fit well with the experimental data, especially in the case of perfusion in MRI T2-w. Always verify the quality of the adjustment when you choose your AIF (see next section).

**III.A.e. Definition of AIF**

AIF = Arterial Input function.

This parameter is very important for the quantitative study of perfusion in T1, CT and T2.

In the software there are 2 types of AIF determination:

- Global AIF: reflects the mean arterial vascularization calculated based on all the pixels of all the images
- Local AIF: AIF is calculated from a group of 9 voxels called ‘arterial’.

By the way, there are 2 ways to determine AIF

- Automatically by LC on

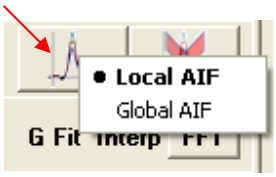
- Semi-automatically : user selects on image of voxels assumed ‘arterial’.

***It is strongly recommended to use the semi-automatic method with the local determination of AIF.***

### III.A.e.1. Global/local determination

To use a global AIF, RC on ‘AIF’ under the perfusion tab on the left of the screen, then LC ‘global AIF’.

To use a local AIF, RC on ‘AIF’ under the perfusion tab on the left of the screen, then LC ‘local AIF’.




### III.A.e.2. – calculating and displaying AIF

This section describes the semi-automatic method of determining AIF.

If you wish to use the automatic method, skip to point 5 (no reference area).

Choose in the image window on the right the slice representing the polygon of Willis.

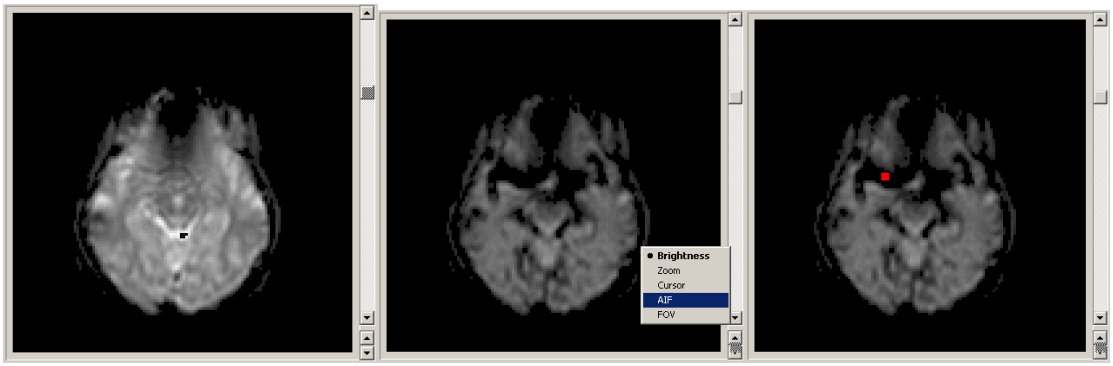
Use the little vertical arrow on the right of the image to scroll through the slice on the T-axis in order to visualize the contrast (the vessels turn black)

RC on the image and LC on the AIF item of the scrolling AIF menu.

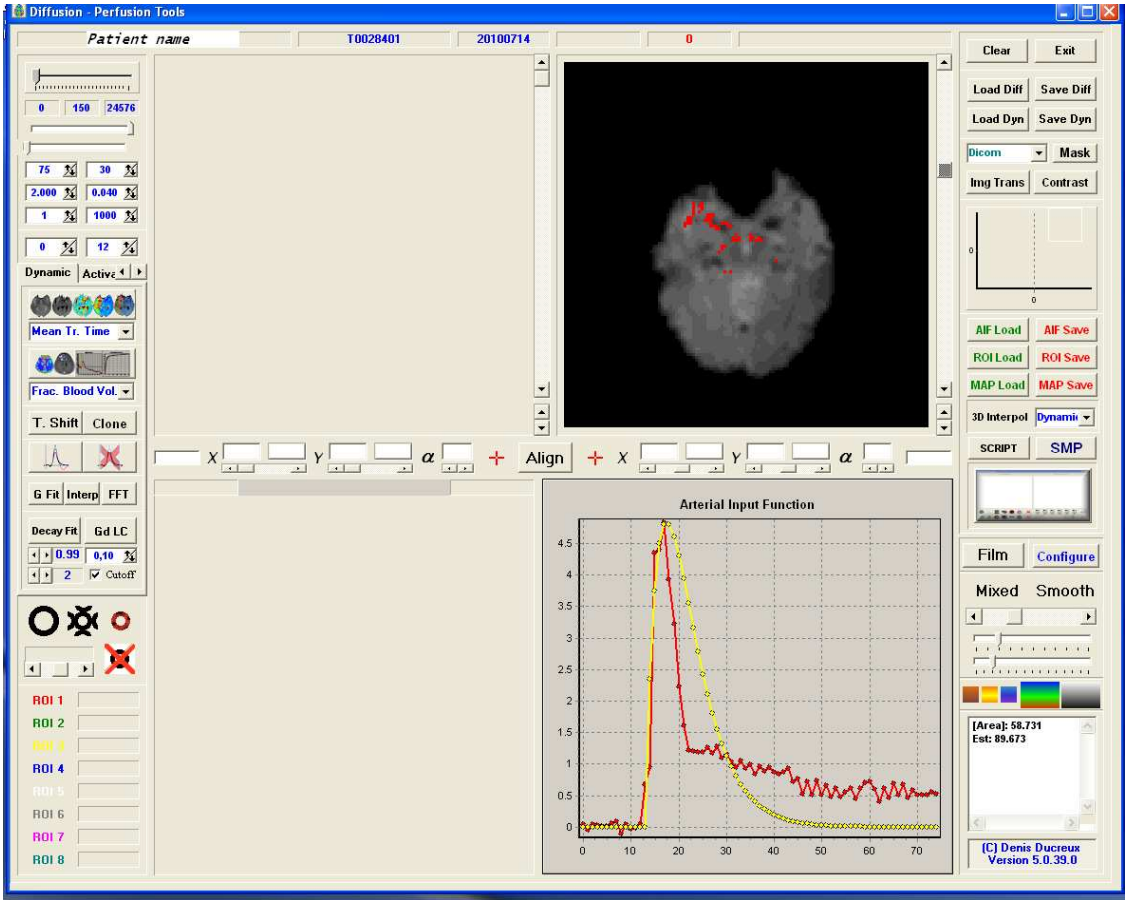
Position your cursor on the vessel and LC on it; a red square representing the arterial reference appears.

LC on ‘AIF’ under the perfusion tab on the left of the screen.

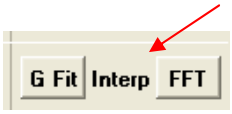
The arterial pixels appear in red on the image; check their intra-arterial position by letting the images scroll by using the big vertical arrow on the right of the image window. Then press F5 while moving your cursor on the image.




Make sure the adjustment of the data is correct If you have activated the ‘GFit’. You must see a blue curve corresponding to the average of the variations of the signal in the selected area (red square on artery). You’ll see a red curve corresponding to the average of variations of all the arterial pixels of all the slices of the study and a yellow curve which is the adjusted curve of the data. Please make sure the yellow curve joins the base line and fits well to the red line in the beginning.

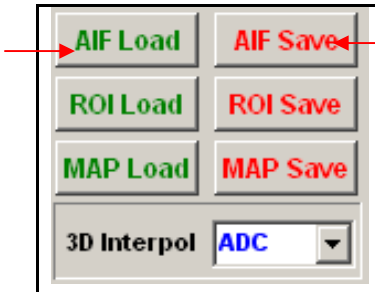



If you are not satisfied with your AIF, LC on 'AIF CL' in the 'perfusion' tab on the left of the screen and begin the procedure from the start.

Some AIF interpolation may be needed, just LC on 'Interp' button 


### III.A.e.3. – Exporting / Importing AIF

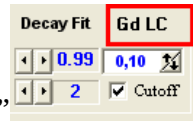
This happens in the Load / Save window on the right of the screen

| | |
|---|---|
|  | LC “AIF Load’ to load an already calculated AIF<br>LC ‘AIF Save’ to save an open AIF<br>You must load an AIF before making perfusion calculations (see below). |

**III.A.f. – Processing**

The software will automatically calculate pixel by pixel the following parameters: TTP, BAT, DR, CBV, CBF, MTT.

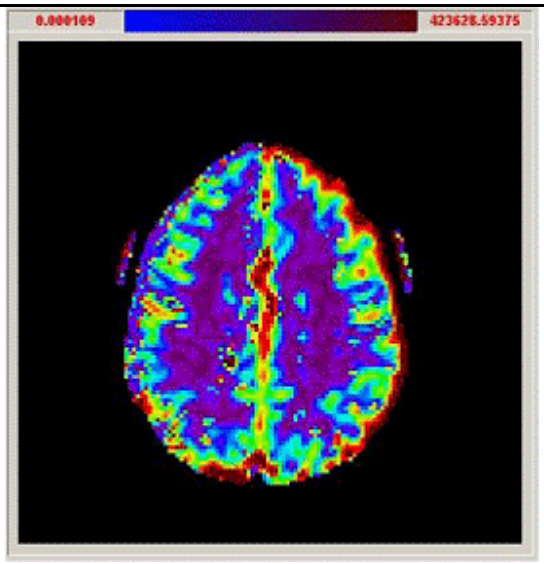
The deconvolution method used to calculate CBF can be selected in the tab ‘Perfusion’ by LC ‘FFT’; you can select FFT, SVD or nothing.


A Gadolinium leakage correction is possible by LC on the button “Gd LC” 

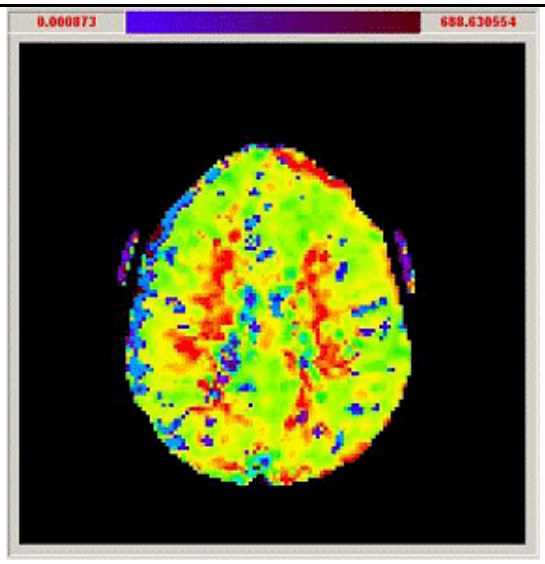

To have T1CDecay correction, LC on the button “Decay Fit”


| | |
|---|---|
| | LC on ‘Compute Perfusion Parameters’ in the tab ‘Dynamic’ on the left of the screen. The calculation will continue.<br>To display the different perfusion maps, LC on the underlying scrolling menu and LC the right item. |

You can also calculate the different perfusion parameters separately. LC on the scrolling menu and LC the item. You must respect the order of the calculations: TTP, the DR, then BAT, then CBV, then CGF, then MTT. You can calculate only CBV and CBF.




CBF (Cerebral Blood Flow)




MTT (Mean Transit Time)

**III.A.g. – Display of results**

Once the calculations have been made, if you want to change the coloring of the window, RC on the calculation window, then choose ‘Brightness’ by RC, then LC on the image while moving your cursor (I.C.a.)

In the same way you can access the other ‘Cursor’ functions for the positioning of ROIs (I.C.d.), ‘Zoom’, and ‘FOV’ for the enlargements (see I.C.c.). When you change FOV of the calculation window, the FOV of the corresponding image window is automatically adjusted.

You can also change the diffusion threshold by moving the position of the ‘Diffusion Threshold’ cursor in the top left of the main screen (see I.C.a.).

CBF – Cerebral blood flow // MTT – Mean Transit Time

### III.A.h. – Export /Import of maps

Once the calculations have been done you can save the results.

The procedure is identical to the one described under II.B.e.

### III.A.i. – Images Overlay

It is very useful to see the ischemic shadow zone to be able to stack diffusion images and perfusion maps.

Once loaded, the perfusion images have to be calculated. You can then load the diffusion images by using the ‘Mixed’ function in section I.E.4.

## III.B. Permeability

Calculation of permeability is based on the bi-compartimental model (refs in section VII) and may use T1-w or T2-w images.

### III.B.a. Selection and loading of images

Before you load your permeability images you need to select the right modality IRM, T2, T1 or CT by clicking the ‘Contrast’ button on the top left of the screen until the correct text appears.

Adjust your ‘Perfusion Threshold” so that you see the parenchymatic structures correctly.

Then load your images as described in I.b.b.

### III.B.b. – Definition of the zones of analysis

Calculation of permeability uses adjustment algorithms of Levenberg-Marquard and can turn out to be a very long process. It is therefore necessary to define a zone of analysis by outlining it manually and to eliminate the rest of the image.

### III.B.b.1. – Outlining

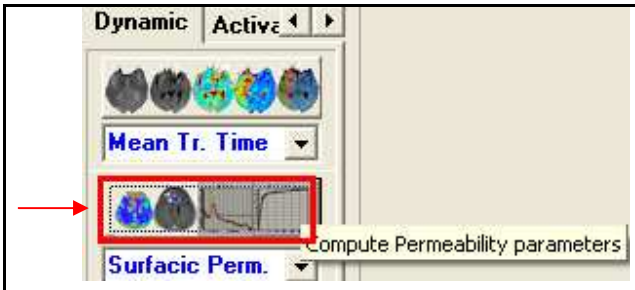
Outlining is based on the principle explained in section I.D.f. – only keep what needs to be analyzed.

### III.B.b.2. Export/Import of areas

Outlined areas behave as ROI and can be loaded or saved as described in section I.D.d.

### III.B.c. – Processing

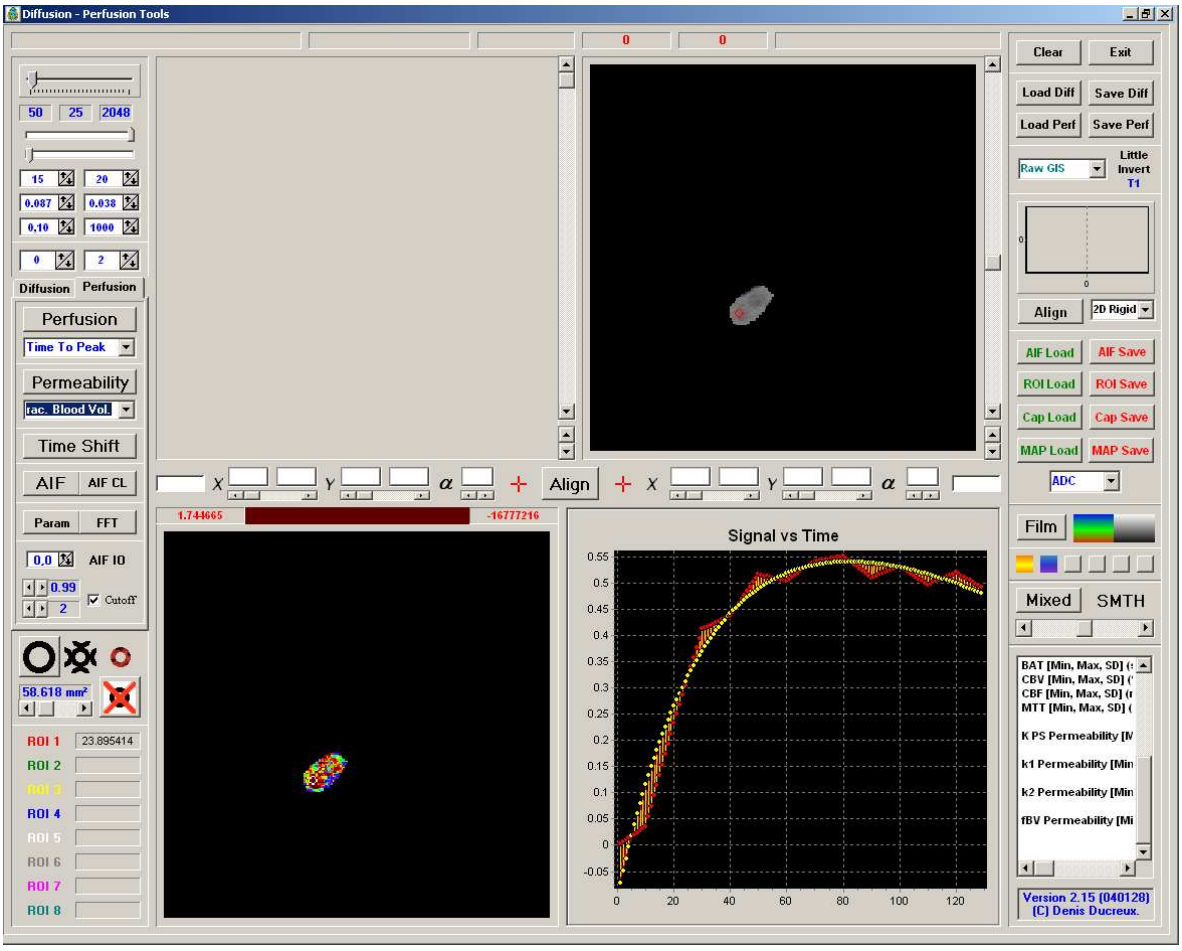
The software automatically calculates the following parameters pixel by pixel: KPS (Permeability of the surface), K1, K2, K Total and fBV.

| | |
|---|---|
|  | LC on permeability under the "Perfusion' tab on the left of the screen. Calculation will follow.<br>To display the different permeability maps, LC on the underlying scrolling menu and LC the chosen item. |

You can also treat the different permeability parameters separately; LC on the scrolling menu and LC the item.

### III.B.d. Display of results

Once the calculations have been made, if you want to change the coloring of the window, RC on the calculation window, then choose ‘Brightness’ by RC, then LC on the image while moving your cursor (I.C.a.)




In the same way you can access the other ‘Cursor’ functions for the positioning of ROIs (I.C.d.), ‘Zoom’, and ‘FOV’ for the enlargements (see I.C.c.). When you change FOV of

the calculation window, the FOV of the corresponding image window is automatically adjusted.

You can also change the diffusion threshold by moving the position of the 'Diffusion Threshold' cursor in the top left of the main screen (see I.C.a.).
The permeability map is displayed in the calculation window on the bottom left. An average curve of maximum reinforcement is then drawn in the curves window. This curve corresponds to the variation of the signal in time of pixel group 9 having the maximum concentration of contrast.
If you position a ROI on the analysis zone, an average curve of reinforcement of the signal is drawn in the curves window (in red) and is adjusted by the bi-compartimental model (in yellow). Please check the adjustment quality.

**III.B.e. – Export/Import of the maps**

Once the calculations have been made, you can save the results. The procedure is identical to the one described in section II.B.e.

**III.B.f. Stacking of images**

To see the zone of ischemic shadow it is very useful to be able to stack diffusion images and perfusion maps. Once loaded the perfusion images need to be calculated. Then load the diffusion images and use the 'MIXED' function described in section I.E.

## III.C. – Flow

The calculation of flow is based on the MRI acquisitions in phase contrast (see refs in Annex).

The calculation method is very similar to the one described in section III.A.

### III.C.a. Selection and loading of images

See section I.B. and I.B.d.

### III.C.b. – Definition of analysis zones

To estimate the flow parameters, you need to position a ROI on the analysis zone and an ROI on the reference zone.

### III.C.b.1. – Reference zone

The reference zone needs to be selected in a region of moderate noise without systolic-diastolic signal variation.

The zone uses the semi-automatic local AIF principles.

RC on the image window on the right, then LC on 'AIF', then LC on the part of the image that serves as reference zone. You can have your images scroll by with help of the large vertical arrow to the right of the image window.

### III.C.b.2. – Analysis zones

Are the zones corresponding to the ROIs. Please refer to section I.D.

### III.C.b.3. Importing/Exporting of analysis zones

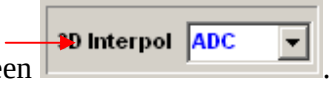
Please see sections I.D. and III.A.e.3.

### III.C.c. Display of results

Once the reference areas and analysis areas have been positioned, the calculation of the parameters of flow happens immediately and is displayed in the results window on the bottom right of the screen (see I.D.).

## III.D. – Activation

Calculating fMRI activation is found under the 'Activation' tab on the left of the screen.

. Computing activation map requires loading data in the right format and setting the paradigm scheme. To avoid motion artifacts, a motion correction has to be performed, similarly to what was described in section III.A.b. If you want to perform inter or intra-subjects comparison, a co-registration to a model has to be performed. Next you have to set the condition you whish to test by setting the condition number in the appropriate filed. Then an automated pre-processing of data is made using a Gaussian spatial and temporal smoothing. fMRI map appear overlayed on the dynamic series. You may want to use other anatomy or reference file. This can be done either using volumic mapping (for volume anatomy) or using the '3D Interpol' button on the right side of the screen 


.

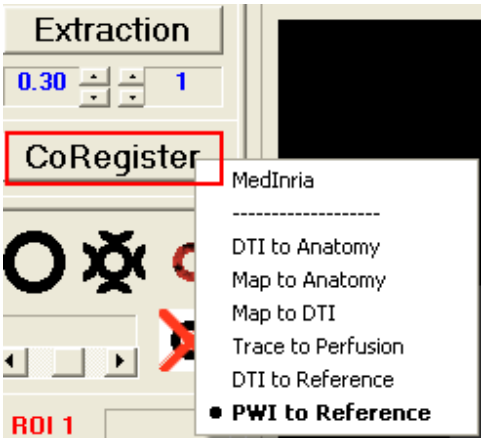
Note that only bloc paradigm with fixed SOA can be processed, but you can choose to compare 2 of the up to 999 conditions. Blocs are convolved with HRF.

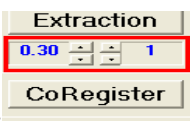
### III.D.a. Selection and loading of images

Images have to be by LC on the “load activation serie” in the Network Database.

### III.D.b. – Motion correction / co-registration

The motion correction is performed using the ‘Re-Align’ button as described in section III.A.b. Co-registration to a model file is performed by RC on ‘Co-Register’ in the ‘MPR/3D’ tab, then LC on ‘PWI to Reference’, then LC on ‘Co-register’. Previously you have to save the model file in GIS format. DPTools will ask you which file you want to use as a model, then perform the co-registration.




By modifying the number on the left of the screen under “extraction” , you choice extraction power thereshold. 

### III.D.c Setting the Paradigm Scheme and the Conditions to test

#### III.D.c.1. – Paradigm Scheme

The Paradigm scheme is presented using a matrix style forme, with on the left cell the condition number, and on the right cell, the condition duration

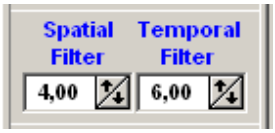
. You can add data using the scrolls.

#### III.D.c.2. Setting the conditions to test

Below the paradigm box are fields where you have to set the conditions numbers you want to test

. Rest condition = 0.

### III.D.d. Automated Activation processing

You can set the temporal and spatial Gaussian smoothing 

before LC on the ‘Activation’ button

. Defaults values are twice TR for temporal and twice slice thickness for spatial.

After LC on the ‘Activation’ button, the map is overlayed on the dynamic series.

**III.D.e. Saving maps:**

The procedure is identical to the one described under II.B.e. You only have to select the 'P.Stats' field for activation maps.

For group studies, you can perform additional statistics on the saved fMRI maps (for example, mean or Z Score). This can be done in the 'Statistics' tab, using the statistics combo

. See chapter IV.

**III.D.f. Displaying maps on volumic / reference images**

You can display maps on 2D references files (such as FLAIR, T2, etc…). This can be done after having saved the activation map in GIS format, then LC on the 'Clear' button, then selecting the 'MRI Anatomy' type by RC on the 'Contrast' button on the right side of the screen. Next you have to set the correct slices number in the 'Serie Slices' section in the upper left part of the screen, as described previously, and setting the 'Serie Phases' to 1.

Then import your files. LC on the '3D Interpol' button, and LC on 'Load Map' to import previously saved activation map. Map will be overlayed on the reference images.

You can also coregister maps on a volumic anatomy file. This file has to be saved in GIS format, for example after the cortex extraction procedure, you can LC on 'Save Dyn', select GIS, and save the volume file.

To perform the coregistration, you need as well a model file of the original fMRI data. This model file has to be in GIS format. After importing the fMRI data, save them using the same process (‘Save Dyn’ button and ‘GIS’ format’).
Once you have all your 3 files (anatomy, fMRI model and map) in GIS format, then click on the ‘Statistic’ tab near the ‘Activation’ tab, and LC on ‘Vol. Mapping’. The map will be coregistered to the volume with identical dimensions and voxel thickness.

This procedure is available for all the maps generated with DPTools (DTI, PWI, aso…).

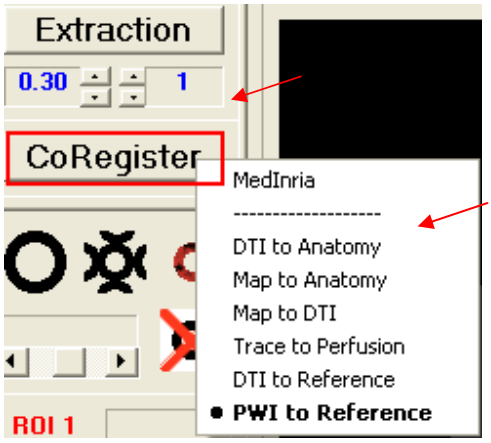
# Chapter IV: Statistics:

The statistical operations refer to the image series of diffusion, perfusion and the maps. It is possible to calculate Mean / Min / Max / SD on several series or maps and to calculate the Z Score, $Chi^2$, Pearson, Difference between series or maps.

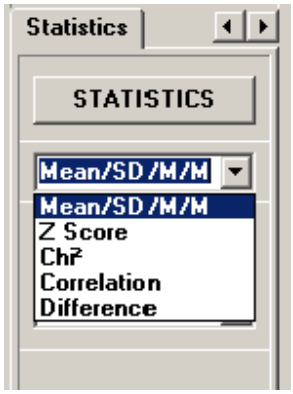
## IV.A. Preparation of the series

Before doing the statistical calculations the series need to be coregistered in comparison with a template. It is possible to create one's own template by averaging several series, all coregistered on one single series.

## IV.B. Coregistration

| | |
|---|---|
|  | Choose the type of coregistration by RC on 'Coregister' under the 'MPR/3D' tab and then load the images to be coregistered (DTI or anatomical).<br>You need a GIS template to be able to coregister your series onto that template. It is possible to create one by saving in GIS format loaded images in dicom for example.<br>Select 'DTI to reference' or 'PWI to reference' and LC on 'Coregister'. |

Once your series have been all coregistered, place them in the same folder on the hard disk and go to the tab ‘Statistics’ and select Mean / Min / Max / SD’, then LC on ‘STATISTICS’.




The files with average, minimum, maximum and standard deviation will be created in the folder of your coregistered series.

By modifying the number above button “Gaussian Smth”, you choice source scaling factor (thereshold). LC on the button “Gaussian smth” to apply smooth Gaussian.

## IV.C. Map creation:

Every coregistered series will be treated separately and the maps resulting from this series will be saved in the same folder.

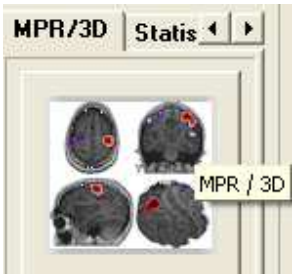
Likewise, you can do statistical calculations based on maps. The generated maps will be saved in the folder of your data.

## IV.D. Importing and thresholding

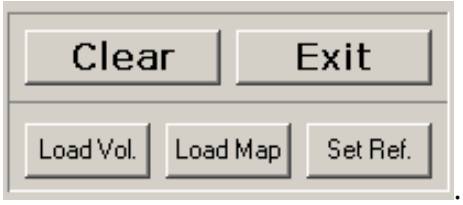
| | |
|---|---|
| | To visualize the statistical maps, you first need to load a visualization support (generally the coregistered series).<br>Then you must load the statistical maps (‘D. Stats’ or ‘P. Stats’) in the ‘Map Load’ on the right of the screen.<br>The threshold will be determined as described in section I.C.a. |

## IV.E. MPR / 3D Surfacic reconstructions

After having saved anatomy and processed map (using the ‘Vol. mapping’ button), you can perform multiplanar reconstructions by LC on the ‘MPR / 3D’ button




in the ‘MPR/3D’ tab. Another window will show up.

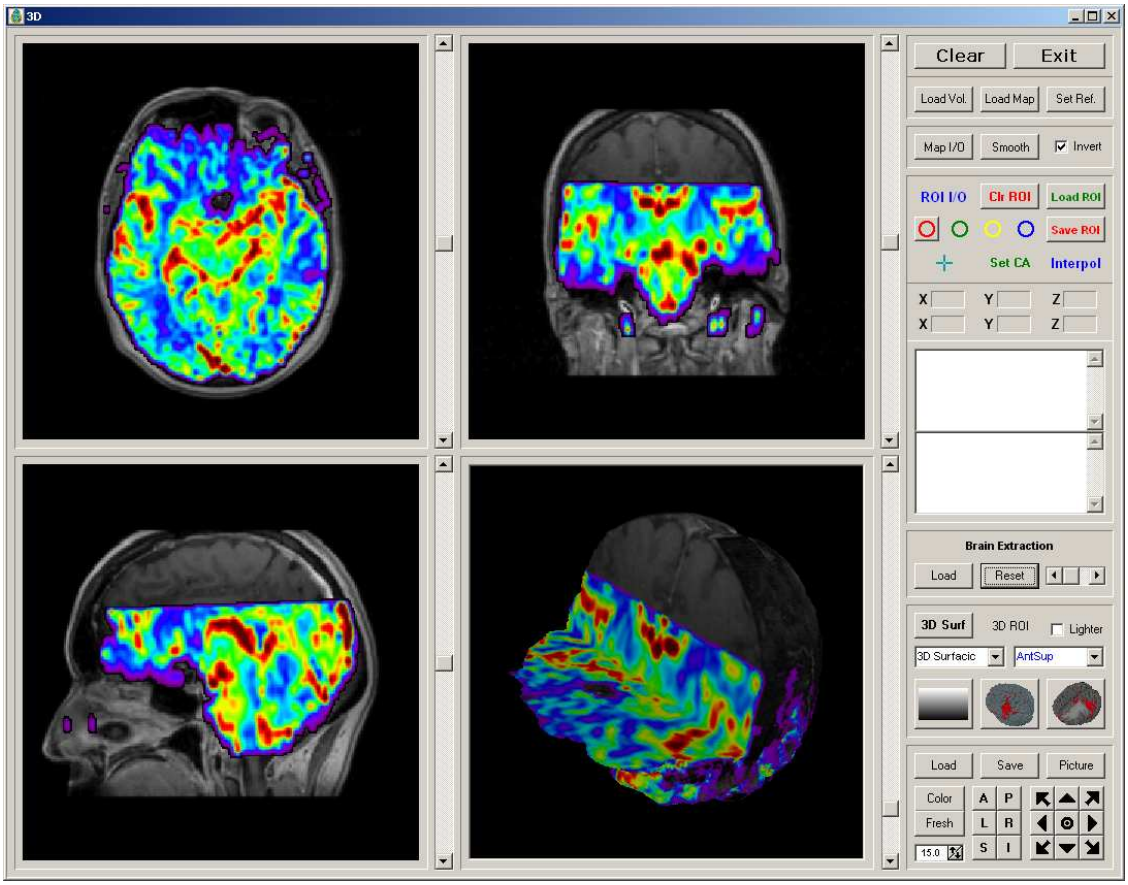
You can also load anatomic files by LC on the ‘Load Vol.’ button, and load maps by LC on the ‘Load Map’ button (GIS format). 


.

Data are smoothed using a Gaussian filter. To deactivate the smoothing, please LC on the ‘Smooth’ button

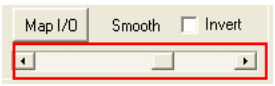
before loading maps .

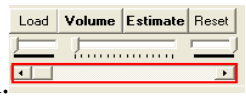
If your map file has a different slice thickness or a different slices number compared to your volume file, you will have to set the reference slice from which the map will be overlayed on anatomy. This slice has to be the top first one.




By RC on the images, you can select between ‘Brightness’, ‘Cursor’, ‘Zoom’, and ‘Map Window’. These functions are similar to those reported earlier in the text.

You can also load previous volume and maps by clicking on ‘Load Vol.’ and ‘Load Map’ buttons, and display maps by LC on the ‘Map I/O’ button on the right of the screen.

You have a bar under this button to adapt the rear projection of the map on the anatomical image. 


You adapt the image visualization (anatomical image and map) with horizontal bar above ‘3D surf’ button, on the right of the screen. 


If your volume reconstruction looks inverted, LC on the ‘Invert’ checkbox

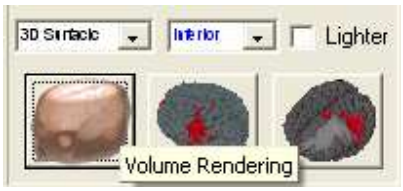
on the right of the screen.

To perform a 3D surfacic reconstruction, you need to have extracted the brain of your volume file (see sections above), then LC on the ‘Brain extraction’ button in the left side of the window

.

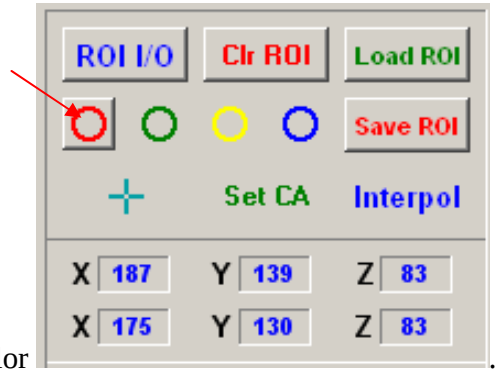
Then LC on ‘MPR/3D’ to open 3D window.

Then LC on ‘Volume Rendering’ to have the 3D reconstruction.



The MRIcroGL open a new window with the result.

*Setting ROIs :*

You can set up to 4 simultaneous 3D ROIs. ROI selection is made by LC on the ROI color 

.

To make ROI on the slice: “shift left + LC”. Verify that your mouse is in ‘cursor’ mode, RC if you need to change. On the right on the screen, the ROI data are indicated.


Coordinates of ROI are reported in mm and in voxels from the CA location (if CA previously set).

By LC on , crossbar is shown. You can Load or Save ROI in Analyze format by LC on the appropriate button. You can enable/disable ROI by LC on

.

You can also clear only the selected ROI by LC on

if

is up, and clear all ROIs if

is down.

Visualizing a ROI volume is made by LC on

after have make ROI on some different slices in axial.

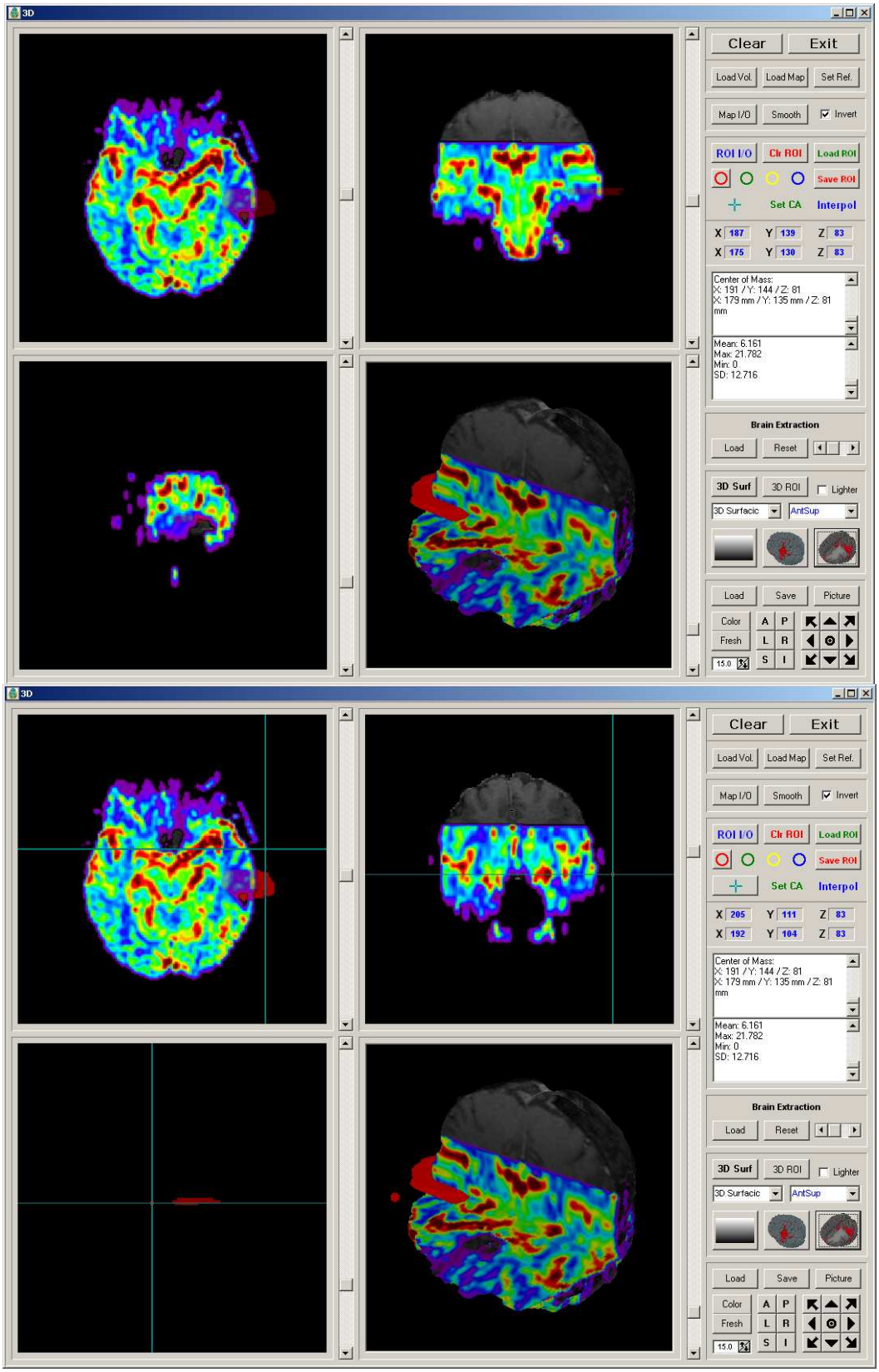
Possibility to push F6 or F7 once while moving the cursor of the mouse on the pertinent image window.

- F3: keeps what has been circled and erases the rest on the visible
- F4 : keeps what has not been circled and erases the rest on all the slices
- F6: keeps what has been circled and erases the rest on the visible slice in the whole volume
- F7 : keeps what has not been circled and erases the rest on all the slices in the whole volume

Visualizing ROI in 3D is made by LC on

after have reconstructed the brain. ROI measurements are visible in the ROI reports windows, and can be saved by typing ‘F1’ key and moving the mouse on it.

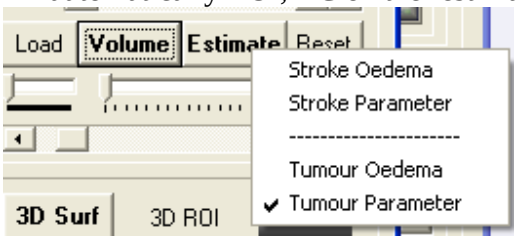
If CrossBar is enabled, then you can see the cursor location in the 3D window.


3D
Clear
Exit
Load Vol.
Load Map
Set Ref.
Map I/O
Smooth
Invert
ROI I/O
Clr ROI
Load ROI
Save ROI
Set CA
Interpol
X 187 Y 139 Z 83
X 175 Y 130 Z 83
Center of Mass:
X: 191 / Y: 144 / Z: 81
X: 179 mm / Y: 135 mm / Z: 81
mm
Mean: 6.161
Max: 21.782
Min: 0
SD: 12.716
Brain Extraction
Load
Reset
3D Surf
3D ROI
Lighter
3D Surfacic
AntSup
Load
Save
Picture
Color
A
P
Fresh
L
R
S
I
15.0
3D
Clear
Exit
Load Vol.
Load Map
Set Ref.
Map I/O
Smooth
Invert
ROI I/O
Clr ROI
Load ROI
Save ROI
Set CA
Interpol
X 205 Y 111 Z 83
X 192 Y 104 Z 83
Center of Mass:
X: 191 / Y: 144 / Z: 81
X: 179 mm / Y: 135 mm / Z: 81
mm
Mean: 6.161
Max: 21.782
Min: 0
SD: 12.716
Brain Extraction
Load
Reset
3D Surf
3D ROI
Lighter
3D Surfacic
AntSup
Load
Save
Picture
Color
A
P
Fresh
L
R
S
I
15.0

Modify the thresholds to make appeared the mask with horizontal bar on the right of the screen

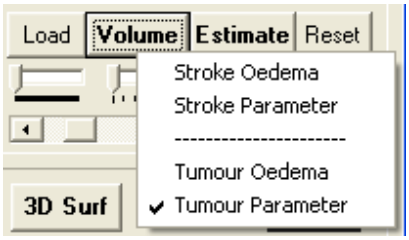
.

An automatically ROI, RC on the ‘estimate’ button to choice the typ of region

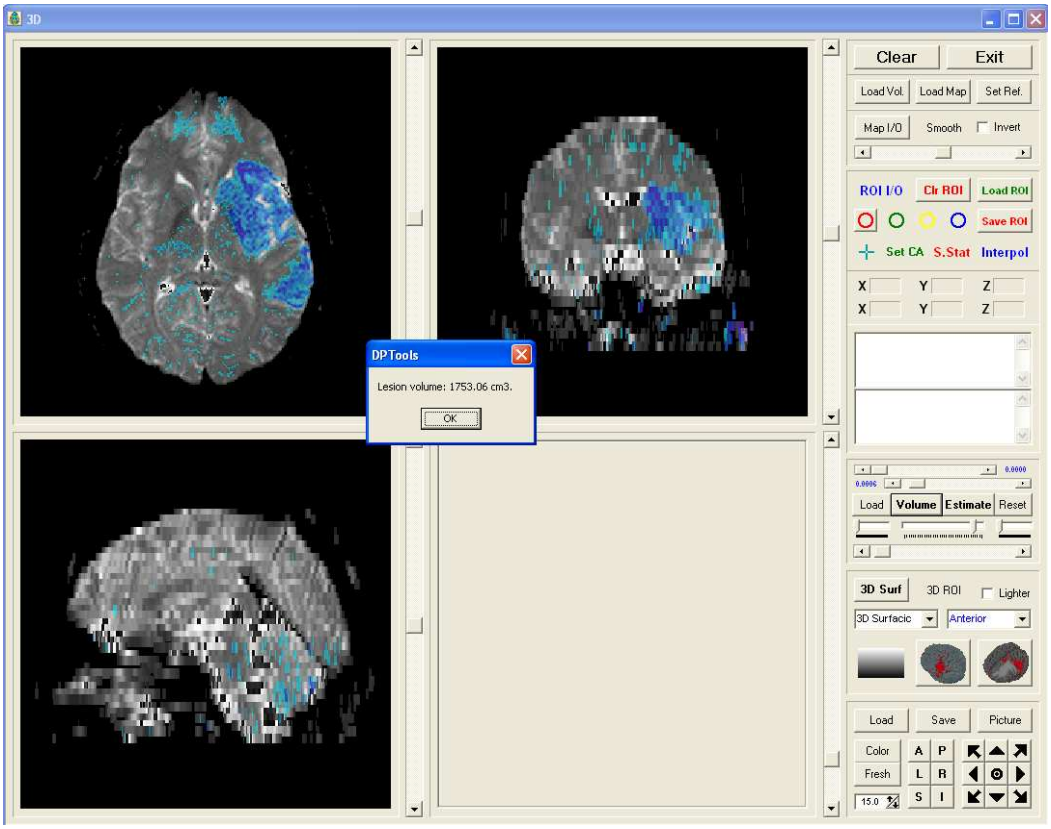



Then LC on the ‘estimate’button. The results are on the images.

You choice volume selection by RC on the ‘Volume’ button




Once the contrast adapted, select volume on the right of the screen:

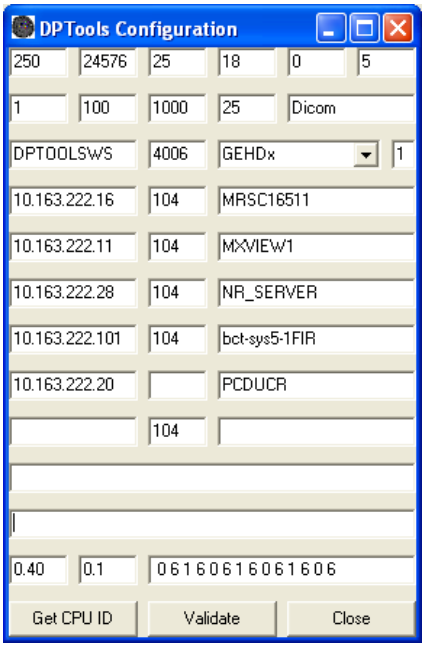

3D
Clear
Exit
Load Vol.
Load Map
Set Ref.
Map I/O
Smooth
Invert
ROI I/O
Clr ROI
Load ROI
Save ROI
Set CA
S.Stat
Interpol
X
Y
Z
X
Y
Z
DPTools
Lesion volume: 1753.06 cm3.
OK
Load
Volume
Estimate
Reset
3D Surf
3D ROI
Lighter
3D Surfacic
Anterior
Load
Save
Picture
Color
A
P
Fresh
L
R
S
I

.

# V. DPTools Preferences

Preferences can be set in DPTools using the 'DPToolsRegistration.exe' software, found either on the website (http://www.fmritools.org), or in the '\DPTools\bin' folder of your installation directory.

This software can set default values of b diffusion gradient, perfusion slices, paradigm scheme, aso…. All fields have hint text as description.




The software generates the dptools.ini file, found in the '\DPTools\bin' directory.

```
# DPTools Ini file - Do not change lines order !
# RAMDrive Letter - If none, keep it blank !

# Diffusion Threshold
100
# Diffusion b value
1000
# DTI directions
25
# Perfusion Low Threshold
250
```

```
# Perfusion High Threshold
24576
# Perfusion Phases
25
# Perfusion Slices
18
# Perfusion SA Start
0
# Perfusion SA Duration
5
# Image Format
Dicom
# Perfusion Gamma Fitting On/Off
1
# DPTools Running Key

# DPtools Tensor Extension
PhilipsKB
# PC AE Title
NRDPTNVISUDD
4006
#Node 1 IP and Port
MRSC16511
10.163.222.16
104
#Node 2 IP and Port
MXVIEW1
10.163.222.11
104
#Node 3 IP and Port
NR_SERVER_2
192.168.128.25
4006
#Node 4 IP and Port
NRSRVDIAG
10.163.222.220
4006
#Node 5 IP and Port
MNAVDICOMQR
10.163.222.245
104
#Node 6 IP and Port
BCT-NRMACDD
10.163.222.248
4096
#SMP
1
#TempCor
0.40
#AutoCor
0.1
#Paradigm
14
0
6
1
6
0
6
1
6
0
6
1
6
0
6
```

# VI. DPTools DTI Gradients Scheme

DTI Gradients scheme can be set in DPTools using a text file found in the '\DPTools\bin' folder of your installation directory. All gradient file names have to begin with 'Gradients'. For exemple here is the 'GradientsSiemensOld.txt' file:

```
Axial
Sagittal
Coronal
12
6
0.0 0.707 0.707
0.0 -0.707 0.707
0.707 0.0 0.707
0.707 0.0 -0.707
0.707 0.707 0.0
0.707 -0.707 0.0
12
1.000000 0.414250 -0.41425
1.000000 0.414250 -0.41425
1.000000 -0.414250 0.41425
1.000000 0.414250 0.41425
0.414250 0.414250 1.0
0.414250 1.000000 0.41425
0.414250 1.000000 -0.41425
0.414250 0.414250 -1.0
0.414250 -0.414250 -1.0
0.414250 -1.000000 -0.41425
0.414250 -1.000000 0.41425
0.414250 -0.414250 1.0
```

---

Axial

Sagittal

Coronal

This section defines the order of the rotation matrix to be performed to the gradients set. It depends on your MRI system.

---

12

The total number of available directions

---

```
6
0.0 0.707 0.707
0.0 -0.707 0.707
0.707 0.0 0.707
0.707 0.0 -0.707
0.707 0.707 0.0
0.707 -0.707 0.0
12
1.000000 0.414250 -0.41425
1.000000 0.414250 -0.41425
1.000000 -0.414250 0.41425
1.000000 0.414250 0.41425
0.414250 0.414250 1.0
0.414250 1.000000 0.41425
0.414250 1.000000 -0.41425
0.414250 0.414250 -1.0
0.414250 -0.414250 -1.0
0.414250 -1.000000 -0.41425
0.414250 -1.000000 0.41425
0.414250 -0.414250 1.0
```

The number of directions followed by the x y z gradients values.

# VII. References

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*Rosen BR, Belliveau JW, Buchbinder BR, McKinstry RC, Porkka LM, Kennedy DN, Neuder MS, Fisel CR, Aronen HJ, Kwong KK, et al. Contrast agent and cerebral hemodynamics. Magn Res Med 1991;19:285-292*

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*Abstract submitted and accepted to the "18th Annual Radiology Research Symposium".*

*Pierre Fillard, John Gilmore, Weili Lin, Guigo Gerig, "Quantitative Analysis of White Matter Fiber Properties along Geodesic Paths",*
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*accepted to MICCAI 2003 conference (avril 2003).*

Dongrong Xu, Susumu Mori, Meiyappan Solaiyappan, Peter C. M. van Zijl and Christos Davatzikos. *A Framework for Callosal Fiber Distribution Analysis.*

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***T1 Permeability algorithms*** based on:

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*Patlak CS, Goldstein DA, Hoffman JF. The flow of solute and solvent across a two-membrane system. J Theor Biol 1963;5:426–442*

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***T2 permeability algorithm patent WO/2008/132386***

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*Smith, S. (2000a). Robust automated brain extraction. NeuroImage. submitted.*

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All other routines and algorithms developped by Denis Ducreux.